

72182

STIC-Biotech/ChemLib

From: Turner, Sharon  
Sent: Wednesday, July 31, 2002 9:12 AM  
To: STIC-Biotech/ChemLib  
Subject: 08948131

Please search CDB and Interference files

08948131

Oligomer search SEQ ID NO:1

Thanks,  
Sharon L. Turner, Ph.D.  
USPTO  
CM1-10B09  
Mailroom 10C01  
Biotechnology GAU 1647  
(703) 308-0056

Edward Hart  
Technical Info. Specialist  
STIC/Biotech  
CMI 6B02 Tel: 305-9203

8210-9-97

Searcher: \_\_\_\_\_  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: 7/31/02  
Date Completed: 7/31/02  
Searcher Prep/Review: \_\_\_\_\_  
Clerical: \_\_\_\_\_  
Online time: \_\_\_\_\_

TYPE OF SEARCH:

NA Sequences: \_\_\_\_\_  
AA Sequences: 1  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)

STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: RDS  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_

This Page Blank (uspto)

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 31, 2002, 15:03:45 ; Search time 30.19 Seconds  
(without alignments)  
110.375 Million cell updates/sec

Title: US-08-948-131-1

Sequence: 1 AONTARIGEPYVAKCKGAPKPPQRLKWK 30

Scoring table: OLIGO  
Gapop 60.0, Gapext 60.0

Searched: 747574 seqs, 111073796 residues

Word size: 0

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database: A\_Geneseq\_032802.\*

```

1: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT.*
4: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT.*
5: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1984.DAT.*
6: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1985.DAT.*
7: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1986.DAT.*
8: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1987.DAT.*
9: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1988.DAT.*
10: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1989.DAT.*
11: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1990.DAT.*
12: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1991.DAT.*
13: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1992.DAT.*
14: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1993.DAT.*
15: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1994.DAT.*
16: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT.*
17: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1996.DAT.*
18: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT.*
19: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT.*
20: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	100.0	30	20	AAV09349
2	30	100.0	30	21	AAV52134
3	30	100.0	30	18	AAW44200
4	30	100.0	318	18	AAW33754
5	30	100.0	332	21	AAV52130
6	30	100.0	340	18	AAW44199
7	30	100.0	340	18	AAW33753
8	30	100.0	404	22	AAW81925
9	16	53.3	16	18	AAW44214
10	16	53.3	16	18	AAW33768
11	15	50.0	15	18	AAW44208

12	15	50.0	15	18	AAW33762
13	13	43.3	30	20	AAV09350
14	11	36.7	30	20	AAV09351
15	10	33.3	10	18	AAW44209
16	10	33.3	10	18	AAW44201
17	10	33.3	10	18	AAW33763
18	10	33.3	10	18	AAW33755
19	10	33.3	10	20	AAV09353
20	10	33.3	10	21	AAV52135
21	10	33.3	30	20	AAV09352
22	9	30.0	30	18	AAW23337
23	7	23.3	178	22	AAW36499
24	7	23.3	237	22	ABB67569
25	7	23.3	742	22	ABB59085
26	6	20.0	10	18	AAW27362
27	6	20.0	10	20	AAW92647
28	6	20.0	39	22	AAO09419
29	6	20.0	47	22	AAO11787
30	6	20.0	49	22	ABB42915
31	6	20.0	49	22	ABB26166
32	6	20.0	49	22	AAW63816
33	6	20.0	49	22	AAW76630
34	6	20.0	49	22	AAW36735
35	6	20.0	61	22	ABB15264
36	6	20.0	78	22	AAU52300
37	6	20.0	86	22	AAO03946
38	6	20.0	92	22	AAO08061
39	6	20.0	99	22	AAU55509
40	6	20.0	105	21	AAW57767
41	6	20.0	114	22	AAW91827
42	6	20.0	116	21	AAW41577
43	6	20.0	116	22	AAO05586
44	6	20.0	139	22	AAW66290
45	6	20.0	139	22	AAO08263

#### ALIGNMENTS

RESULT 1  
AAV09349 standard; peptide: 30 AA.  
XX  
AC AAV09349;  
DT 09-JUL-1999 (first entry)  
XX  
DE Human RAGE V-domain peptide SEQ ID NO:1.  
XX  
KW RAGE; V-domain; receptor for advanced glycation endproduct;  
KW ligand binding site; amyloid-beta; Alzheimer's disease; Down's syndrome;  
KW sensitivity; renal failure; hyperlipidaemic atherosclerosis; dementia;  
KW neuronal cytotoxicity; head trauma; amyotrophic lateral sclerosis;  
KW multiple sclerosis; amyloidosis; autoimmune disease; inflammation;  
KW tumour; cancer; male impotence; wound healing; periodontal disease;  
KW neuropathy; retinopathy; nephropathy; neuronal degeneration.  
XX  
OS Homo sapiens.  
XX  
PN WO9918987-A1.  
XX  
PD 22-APR-1999.  
XX  
PF 09-OCT-1998; 98WO-US21346.  
XX  
PR 09-OCT-1997; 97US-0948131.  
XX  
PA (UYCO) UNIV COLUMBIA NEW YORK.  
XX  
PI Lamster I, Schmidt AM, Stern D, Yan SP.  
XX  
DR WPI; 1999-277439/23.  
XX

Human RAGE polypep  
Mouse RAGE V-domain  
Rat RAGE V-domain  
Human soluble RAGE  
Human soluble RAGE  
Human RAGE polypep  
Human RAGE polypep  
Human RAGE V-domain  
Human Receptor to  
Bovine RAGE V-domain  
N-terminal sequenc  
Acinetobacter sp.  
Drosophila melanog  
Residues 138-147 o  
Human HAI-1 peptid  
Human polypeptide  
Human polypeptide  
Peptide #10421 enc  
Protein #8165 enc  
Human brain expres  
Human bone marrow  
Peptide #10772 enc  
Human nervous syst  
Propionibacterium  
Human polypeptide  
Human polypeptide  
Propionibacterium  
Human ORFX ORF1341  
Human polypeptide  
Human polypeptide  
Human polypeptide

PT New peptides based on an advanced glycation end product receptor are  
 PT useful for treating Alzheimer's disease and Down's syndrome  
 PS Claim 2; Page 78; 101pp; English.

CC The present invention describes novel isolated peptides (1) having an  
 CC amino acid sequence corresponding to an amino acid sequence of a  
 CC V-domain of a receptor for an advanced glycation end product (RAGE).  
 CC Also described are methods for: (1) inhibiting an amyloid-beta peptide  
 CC (ABP) interaction with a receptor for RAGE when the receptor is on the  
 CC surface of a cell; (2) inhibiting degeneration of a neuronal cell; (3)  
 CC inhibiting formation of an ABP fibril on a cell; (4) inhibiting  
 CC extracellular assembly of an ABP into a fibril; (5) inhibiting  
 CC aggregation of ABP on the surface of a cell; (6) inhibiting infiltration  
 CC of a microglial cell into senile plaques; (7) inhibiting activation of a  
 CC microglial cell by an ABP; (8) treating a subject with a condition  
 CC associated with an interaction of an ABP with a receptor for RAGE on a  
 CC cell; (9) evaluating the ability of an agent to inhibit binding of an  
 CC ABP with a V-domain of a receptor for RAGE on the surface of a cell; (10)  
 CC inhibiting activation of a NF-kappaB gene in a cell; (11) inhibiting  
 CC periodontal disease in a subject; (12) inhibiting an RAGE's interaction  
 CC with a receptor for RAGE when the receptor is on the surface of a cell;  
 CC and (13) treating a subject with a condition associated with an  
 CC interaction of an RAGE with a receptor for RAGE on a cell. The methods  
 CC can be used for treating conditions associated with an interaction of an  
 CC APP or an RAGE with a receptor for RAGE, e.g. diabetes, Alzheimer's  
 CC disease, senility, renal failure, hyperlipidaemic atherosclerosis,  
 CC neuronal cytotoxicity, Down's syndrome, dementia associated with head  
 CC trauma, amyotrophic lateral sclerosis, multiple sclerosis, amyloidosis,  
 CC an autoimmune disease, inflammation, a tumour, cancer, male impotence,  
 CC wound healing, periodontal disease, neuropathy, retinopathy, nephropathy  
 CC or neuronal degeneration.

SQ Sequence 30 AA;

Query Match 100.0%; Score 30; DB 20; Length 30;  
 Best Local Similarity 100.0%; Pred. No. 5.8e-25;  
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONTTARIGEPVLKCKGAPKPPQRLWK 30  
 DB 1 agntarigepvlkckgapkppqrlwk 30

RESULT 2  
 AAY52134  
 ID AAY52134 standard; protein; 30 AA.

XX AAY52134;

XX 28-JAN-2000 (first entry)

XX Human Receptor to AGE (RAGE) amino acid sequence fragment #3.

XX Soluble receptor for advanced glycation endproducts; RAGE; tumour;  
 KM invasion; metastasis; amphoterin; neuron; inhibit; therapy.

XX Homo sapiens.

XX WO954485-A1.

XX 28-OCT-1999.

XX 16-APR-1999; 99WO-US08427.

XX 17-APR-1998; 98US-0062365.

XX (UYCO ) UNIV COLUMBIA NEW YORK.

XX Schmidt AM, Stern D;

XX WPI; 2000-013260/01.

XX Inhibiting tumour invasion or spreading by administration of soluble  
 PT receptor for advanced glycation endproducts -  
 PS Claim 29; Page 62; 88pp; English.

CC This is the amino acid sequence of a fragment of the human soluble  
 CC Receptor for Advanced Glycation Endproducts (RAGE). RAGE interacts with  
 CC a range of physiologically and pathophysiologically relevant ligands  
 CC when considering tumour invasion. In normal developing neurons RAGE  
 CC colocalizes with amphoterin which is a matrix associated polypeptide.  
 CC The expression of both RAGE and amphoterin decreases after birth, but  
 CC both have increased expression in tumours. RAGE polypeptides  
 CC AAY52132-Y52135 are used in the invention in a method for inhibiting  
 CC tumour invasion and metastasis. The method involves inhibiting tumour  
 CC invasion and metastasis via administration of a therapeutically effective  
 CC amount of the pharmaceutical composition containing a RAGE polypeptide.  
 CC The invention also relates to a method for evaluating the ability of an  
 CC agent to inhibit tumour invasion in a local cellular environment. RAGE  
 CC can be administered to a patient in a pharmaceutically acceptable  
 CC carrier.

SQ Sequence 30 AA;

Query Match 100.0%; Score 30; DB 21; Length 30;  
 Best Local Similarity 100.0%; Pred. No. 5.8e-25;  
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONTTARIGEPVLKCKGAPKPPQRLWK 30  
 DB 1 agntarigepvlkckgapkppqrlwk 30

RESULT 3  
 AAM44200  
 ID AAM44200 standard; protein; 318 AA.

XX AAM44200;

XX 14-MAY-1998 (first entry)

XX Human mature receptor to an advanced glycosylation end product.

XX Human; soluble receptor; advanced glycosylation end product; RAGE;  
 KM AGE; antibody; vascular permeability; diabetes mellitus.

XX Homo sapiens.

XX Key Location/Qualifiers

FT MISC-difference 66 /note="encoded by CCR"

XX WO9739125-A1.

XX 23-OCT-1997.

XX 11-APR-1997; 97WO-EP01834.

XX 16-APR-1996; 96US-0633148.

XX (SCHD ) SCHERING PATENTE AG.

XX Hollander DA, Morser MJ, Nagashima M;

XX WPI; 1997-558580/51.

XX N-PSDB; AAV12395.

XX Anti-advanced glycosylation end product polypeptide antibody -  
 PT prevents receptor binding and therefore reduces vascular  
 PT permeability, useful to treat diabetes mellitus

PS Claim 2; Page 42-43; 90pp; English.

XX The present sequence represents a mature human receptor to an advanced  
 CC glycosylation end product (RAGE) polypeptide. The present invention  
 CC describes an isolated antibody (Ab), specifically immunoreactive with  
 CC RAGE. Advanced glycosylation end products (AGE) of proteins are  
 CC non-enzymatically glycosylated proteins, which accumulate in vascular  
 CC tissue in ageing, and at an accelerated rate in individuals with  
 CC diabetes. The Ab, which prevents the interaction between an AGE and its  
 CC receptor (RAGE), reduces vascular permeability. The Ab can be used to  
 CC treat diabetes mellitus symptoms, e.g. microvasculopathy, occlusive  
 CC vascular disorders, neuropathy, nephropathy, retinopathy, haemodialysis  
 CC associated amyloidosis or atherosclerosis. The Ab can also be used for  
 CC the isolation and purification of human RAGE polypeptide.

XX Sequence 318 AA:

Query Match 100.0%; Score 30; DB 18; Length 318;  
 Best Local Similarity 100.0%; Pred. No. 4e-24;  
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AONTARIGEPLVLCCKGAPKPPQRLWK 30  
 ||||||||||||||||||||||||||||  
 DB 1 aqnltarigeplvkcckgapkppqrlwkw 30

#### RESULT 4

AAW33754  
 ID AAW33754 standard; Protein; 318 AA.

AC AAW33754;

DT 08-MAY-1998 (first entry)

DE Human RAGE polypeptide (318 amino acid residues).

XX Advanced glycosylation end-product receptor; RAGE; screening; AGE;

KW vascular permeability; diabetes mellitus; treatment; atherosclerosis;

KW Alzheimer's disease.

XX Homo sapiens.

XX WO9739121-A1.

XX 23-OCT-1997.

XX 11-APR-1997; 97WO-EP01832.

XX 16-APR-1996; 96US-0633147.

XX (SCHD) SCHERING AG.

XX Morser MJ, Nagashima M;

XX WPI; 1997-526458/48.

XX N-PSDB; AAV06518.

XX New soluble advanced glycosylation end-product receptor polypeptide

PT - used for reducing vascular permeability, complications of diabetes

XX etc., also for purification and to screen for modulators

XX Claim 3; Fig 1B; 91pp; English.

XX This is a human advanced glycosylation end-product receptor (RAGE)  
 CC polypeptide (318 amino acid residues). The RAGE polypeptides and its  
 CC active fragments or their mimetics, inhibit interaction between advanced  
 CC glycosylation end-products (AGE) and a receptor (specifically RAGE). They  
 CC are used to treat diseases associated with AGE/RAGE interaction, such as  
 CC increased vascular permeability, diabetes mellitus (particularly  
 CC complications such as micro- or macro- vasculopathy or occlusive vascular  
 CC disorders such as neuropathy, nephropathy, retinopathy or  
 CC atherosclerosis) or haemodialysis-associated amyloidosis, also activation  
 CC of microglial cells by beta-amyloid peptides in Alzheimer's disease or

CC age-related disorders such as oxidative stress. These RAGE polypeptides  
 CC are also used, when immobilised, to purify AGE from a protein mixture and  
 CC to screen for compounds that are agonists and antagonists of AGE/RAGE  
 CC interaction. They can also be used diagnostically to detect abnormal  
 CC levels of AGE. Antibodies against RAGE polypeptides are useful as  
 CC immunoassay reagents for measurement of RAGE levels, and as inhibitors of  
 CC interaction between AGE and RAGE or other receptors and for purification  
 CC and quantification of RAGE polypeptides. The encoding nucleic acids are  
 CC used to express recombinant RAGE and as probes for isolating related  
 CC genes.

XX Sequence 318 AA:

Query Match 100.0%; Score 30; DB 18; Length 318;  
 Best Local Similarity 100.0%; Pred. No. 4e-24;  
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AONTARIGEPLVLCCKGAPKPPQRLWK 30  
 ||||||||||||||||||||||||||||  
 DB 1 aqnltarigeplvkcckgapkppqrlwkw 30

#### RESULT 5

AA52130  
 ID AA52130 standard; protein; 332 AA.

AC AA52130;

DT 28-JAN-2000 (first entry)

DE Human Receptor to AGE (RAGE) amino acid sequence.

XX Soluble receptor for advanced glycation endproducts; RAGE; tumour;

KW invasion; metastasis; amphoterin; neuron; inhibit; therapy.

XX Homo sapiens.

XX WO954485-A1.

XX 28-OCT-1999.

XX 16-APR-1999; 99WO-US08427.

XX 17-APR-1998; 98US-0062365.

XX (UYCO) UNIV COLUMBIA NEW YORK.

XX Schmidt AM, Stern D;

XX WPI; 2000-013260/01.

XX Inhibiting tumour invasion or spreading by administration of soluble

PT receptor for advanced glycation endproducts -

XX Disclosure; Page 10-11; 88pp; English.

XX This is the amino acid sequence of the human soluble Receptor for  
 CC Advanced Glycation Endproducts (RAGE). RAGE interacts with a range of  
 CC physiologically and pathophysiologically relevant ligands when  
 CC considering tumour invasion. In normal developing neurons RAGE  
 CC colocalizes with amphoterin which is a matrix associated polypeptide.  
 CC The expression of both RAGE and amphoterin decreases after birth, but  
 CC both have increased expression in tumours. RAGE polypeptides  
 CC AA52132-52133 are used in the invention in a method for inhibiting  
 CC tumour invasion and metastasis. The method involves inhibiting tumour  
 CC invasion and metastasis via administration of a therapeutically effective  
 CC amount of the pharmaceutical composition containing a RAGE polypeptide.  
 CC The invention also relates to a method for evaluating the ability of an  
 CC agent to inhibit tumour invasion in a local cellular environment. RAGE  
 CC can be administered to a patient in a pharmaceutically acceptable  
 CC carrier.

SO Sequence 332 AA;

Query Match 100.0%; Score 30; DB 21; Length 332;  
Best Local Similarity 100.0%; Pred. No. 4.2e-24;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AONTARIGEPVLKCKGAPKKPPORLEWK 30  
Db 1 agntarigepvlkckgapkpporlewk 30

RESULT 6

ID AAW44199 standard; Protein: 340 AA.  
XX AAW44199;

DT 14-MAY-1998 (first entry)

DE Human soluble receptor to an advanced glycosylation end product.

KW Human; soluble receptor; advanced glycosylation end product; RAGE;

XX AGE; antibody; vascular permeability; diabetes mellitus.

OS Homo sapiens.

PN WO9739125-A1.

PD 23-OCT-1997.

PF 11-APR-1997; 97WO-EP01834.

PR 16-APR-1996; 96US-0633148.

PA (SCHD ) SCHERING PATENTE AG.

PI Hollander DA, Morser MJ, Nagashima M;

DR WPI: 1997-558580/51.

PT N-PSDB; AAV12394.

PS Claim 2; Page 40-41; 90pp; English.

CC The present sequence represents a soluble human receptor to an advanced  
glycosylation end product (RAGE) polypeptide. The present invention  
describes an isolated antibody (Ab), specifically immunoreactive with  
RAGE. Advanced glycosylation end products (AGE) of proteins are  
non-enzymatically glycosylated proteins, which accumulate in vascular  
tissue in ageing, and at an accelerated rate in individuals with  
diabetes. The Ab, which prevents the interaction between an AGE and it's  
receptor (RAGE), reduces vascular permeability. The Ab can be used to  
treat diabetes mellitus symptoms, e.g. microvasculopathy, occlusive  
vascular disorders, neuropathy, nephropathy, retinopathy, haemodialysis  
associated amyloidosis or atherosclerosis. The Ab can also be used for  
the isolation and purification of human RAGE polypeptide.

SO Sequence 340 AA;

Query Match 100.0%; Score 30; DB 18; Length 340;  
Best Local Similarity 100.0%; Pred. No. 4.3e-24;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AONTARIGEPVLKCKGAPKKPPORLEWK 30  
Db 23 agntarigepvlkckgapkpporlewk 52

RESULT 7

ID AAW33753 standard; Protein: 340 AA.  
XX AAW33753;

DT 08-MAY-1998 (first entry)

DE Human RAGE polypeptide (340 amino acid residues).

KW Advanced glycosylation end-product receptor; RAGE; screening; AGE;  
vascular permeability; diabetes mellitus; treatment; atherosclerosis;  
Alzheimer's disease.

OS Homo sapiens.

PN WO9739121-A1.

PD 23-OCT-1997.

PF 11-APR-1997; 97WO-EP01832.

PR 16-APR-1996; 96US-0633147.

PA (SCHD ) SCHERING AG.

PI Morser MJ, Nagashima M;

DR WPI: 1997-526458/48.

PT N-PSDB; AAV06517.

CC New soluble advanced glycosylation end-product receptor polypeptide  
- used for reducing vascular permeability, complications of diabetes  
etc., also for purification and to screen for modulators

PS Claim 3; Fig 1A; 91pp; English.

CC This is a human advanced glycosylation end-product receptor (RAGE)  
polypeptide (340 amino acid residues). The RAGE polypeptides and its  
active fragments or their mimetics, inhibit interaction between advanced  
glycosylation end-products (AGE) and a receptor (specifically RAGE). They  
are used to treat diseases associated with AGE/RAGE interaction, such as  
increased vascular permeability, diabetes mellitus (particularly  
complications such as micro- or macro- vasculopathy or occlusive vascular  
disorders such as neuropathy, nephropathy, retinopathy or  
atherosclerosis) or haemodialysis-associated amyloidosis, also activation  
of microglial cells by beta-amyloid peptides in Alzheimer's disease or  
AGE-related disorders, such as oxidative stress. These RAGE polypeptides  
are also used, when immobilised, to purify AGE from a protein mixture and  
to screen for compounds that are agonists and antagonists of AGE/RAGE  
interaction. They can also be used diagnostically to detect abnormal  
levels of AGE. Antibodies against RAGE polypeptides are useful as  
immunassay reagents for measurement of RAGE levels, and as inhibitors of  
interaction between AGE and RAGE or other receptors and for purification  
and quantification of RAGE polypeptides. The encoding nucleic acids are  
used to express recombinant RAGE and as probes for isolating related  
genes.

SO Sequence 340 AA;

Query Match 100.0%; Score 30; DB 18; Length 340;  
Best Local Similarity 100.0%; Pred. No. 4.3e-24;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AONTARIGEPVLKCKGAPKKPPORLEWK 30  
Db 23 agntarigepvlkckgapkpporlewk 52

RESULT 8

ID AAB81925 standard; Protein: 404 AA.

```

XX AC AAB81925;
XX
XX DT 15-JUN-2001 (first entry)
XX
XX DE Extracorporeal circulation material receptor protein.
XX
XX DE Extracorporeal circulation; carbonyl stress product; receptor;
XX
XX KM diabetes; vascular lesion; excretory dysfunction.
XX
XX OS Unidentified.
XX
XX PN WO200118060-A1.
XX
XX PD 15-MAR-2001.
XX
XX PF 08-SEP-2000; 2000WO-JP06172.
XX
XX PR 08-SEP-1999; 99JP-0254463.
XX
XX PA (TORA ) TORAY IND INC.
XX
XX PI Shimizu S, Kubota M, Akiyama H, Usui M;
XX
XX DR WPI; 2001-290314/30.
XX
XX PT Material for extracorporeal circulation, applicable in selective
XX
XX PT elimination of diabetic complication factors such as carbonyl stress
XX
XX PT products caused by abnormally promoted carbonyl stress from excretory
XX
XX PT dysfunction in vascular lesions
XX
XX PS Claim 1; Page 31-32; 36pp; Japanese.
XX
XX CC The present invention describes a material for extracorporeal circulation
XX
XX CC which is made from a water-insoluble carrier immobilized with a protein
XX
XX CC having the sequence shown here. The materials of the invention, including
XX
XX CC adsorbents, are for extracorporeal circulation, which are applicable in
XX
XX CC the selective elimination of diabetic complication factors from a body
XX
XX CC fluid, and are therefore useful in treating vascular lesions like
XX
XX CC arteriosclerosis due to carbonyl stress products caused by abnormally
XX
XX CC promoted carbonyl stress from excretory dysfunction.
XX
XX SQ Sequence 404 AA;

Query Match 100.0%; Score 30; DB 22; Length 404;
Best Local Similarity 100.0%; Pred. No. 4.9e-24;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AONTTARIGEPVLKCGARKPPQRLMK 30
   |||||||||||||||||||||||||||
Db 23 agntarigepvlkcgarkppqrlmk 52

RESULT 9
AAW44214
ID AAW44214 standard; peptide; 16 AA.
XX
XX AC AAW44214;
XX
XX DT 14-MAY-1998 (first entry)
XX
XX DE Human soluble RAGE immunologically active fragment SEQ ID NO:18.
XX
XX KM Human; soluble receptor; advanced glycosylation end product; RAGE;
XX
XX KM AGE; antibody; vascular permeability; immunologically active fragment;
XX
XX KM diabetes mellitus.
XX
XX OS Homo sapiens.
XX
XX PN WO9739125-A1.
XX
XX PD 23-OCT-1997.

```

```

XX PF 11-APR-1997; 97WO-EP01834.
XX
XX PR 16-APR-1996; 96US-0633148.
XX
XX PA (SCHD ) SCHERING PATENTE AG.
XX
XX PI Hollander DA, Morser MJ, Nagashima M;
XX
XX DR WPI; 1997-558580/51.
XX
XX PT Anti-advanced glycosylation end product polypeptide antibody
XX
XX PT prevents receptor binding and therefore reduces vascular
XX
XX PT permeability, useful to treat diabetes mellitus
XX
XX PS Claim 2; Page 49; 90pp; English.
XX
XX CC The present sequence represents an immunologically active fragment
XX
XX CC of a soluble human receptor to an advanced glycosylation end
XX
XX CC product (RAGE) polypeptide. The present invention describes
XX
XX CC an isolated antibody (Ab), specifically immunoreactive with
XX
XX CC RAGE. Advanced glycosylation end products (AGE) of proteins are
XX
XX CC non-enzymatically glycosylated proteins, which accumulate in vascular
XX
XX CC tissue in ageing, and at an accelerated rate in individuals with
XX
XX CC diabetes. The Ab, which prevents the interaction between an AGE and it's
XX
XX CC receptor (RAGE), reduces vascular permeability. The Ab can be used to
XX
XX CC treat diabetes mellitus symptoms, e.g. microvasculopathy, occlusive
XX
XX CC vascular disorders, neuropathy, nephropathy, retinopathy, haemodialysis
XX
XX CC associated amyloidosis or atherosclerosis. The Ab can also be used for
XX
XX CC the isolation and purification of human RAGE polypeptide.
XX
XX SQ Sequence 16 AA;

Query Match 53.3%; Score 16; DB 18; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.9e-10;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AONTTARIGEPVLKCG 16
   |||||||||||||||
Db 1 agntarigepvlkcg 16

RESULT 10
AAW33768
ID AAW33768 standard; peptide; 16 AA.
XX
XX AC AAW33768;
XX
XX DT 08-MAY-1998 (first entry)
XX
XX DE Human RAGE polypeptide fragment 14.
XX
XX KM Advanced glycosylation end-product receptor; RAGE; screening; AGE;
XX
XX KM vascular permeability; diabetes mellitus; treatment; atherosclerosis;
XX
XX KM Alzheimer's disease.
XX
XX OS Homo sapiens.
XX
XX PN WO9739121-A1.
XX
XX PD 23-OCT-1997.
XX
XX PF 11-APR-1997; 97WO-EP01832.
XX
XX PR 16-APR-1996; 96US-0633147.
XX
XX PA (SCHD ) SCHERING AG.
XX
XX PI Morser MJ, Nagashima M;
XX
XX DR WPI; 1997-526458/48.

```





CC of microglial cells by beta-amyloid peptides in Alzheimer's disease or  
CC age-related disorders such as oxidative stress. These RAGE polypeptides  
CC are also used, when immobilised, to purify AGE from a protein mixture and  
CC to screen for compounds that are agonists and antagonists of AGE/RAGE  
CC interaction. They can also be used diagnostically to detect abnormal  
CC levels of AGE. Antibodies against RAGE polypeptides are useful as  
CC immunoassay reagents for measurement of RAGE levels, and as inhibitors of  
CC interaction between AGE and RAGE or other receptors and for purification  
CC and quantification of RAGE polypeptides. The encoding nucleic acids are  
CC used to express recombinant RAGE and as probes for isolating related  
CC genes.

CC Sequence 15 AA:

QY Query Match 50.0%; Score 15; DB 18; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.2e-09;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AONTARIGEPLVLK 15  
Db 1 aqntarigeplvlk 15

#### RESULT 13

AAV09350  
ID AAV09350 standard; peptide: 30 AA.

AC AAY09350;

DT 09-JUL-1999 (first entry)

DE Mouse RAGE V-domain peptide SEQ ID NO:2.

XX RAGE: V-domain; receptor for advanced glycation endproduct;  
XX ligand binding site; amyloid-beta; Alzheimer's disease; Down's syndrome;  
XX senility; renal failure; hyperlipidaemic atherosclerosis; dementia;  
XX neuronal cytotoxicity; head trauma; amyotrophic lateral sclerosis;  
XX multiple sclerosis; amyloidosis; autoimmune disease; inflammation;  
XX tumour; cancer; male impotence; wound healing; periodontal disease;  
XX neuropathy; retinopathy; nephropathy; neuronal degeneration.

OS Mus sp.

PN WO9918987-A1.

PD 22-APR-1999.

PF 09-OCT-1998; 98WO-US21346.

PR 09-OCT-1997; 97US-0948131.

PA (UYCO ) UNIV COLUMBIA NEW YORK.

PI Lamster I, Schmidt AM, Stern D, Yan SD;

DR WPI: 1999-277439/23.

XX New peptides based on an advanced glycation end product receptor are  
PT useful for treating Alzheimer's disease and Down's syndrome

PS Claim 3; Page 78; 101pp; English.

CC The present invention describes novel isolated peptides (1) having an  
CC amino acid sequence corresponding to an amino acid sequence of a  
CC V-domain of a receptor for an advanced glycation end product (RAGE).  
CC Also described are methods for: (1) inhibiting an amyloid-beta peptide  
CC (ABP) interaction with a receptor for RAGE when the receptor is on the  
CC surface of a cell; (2) inhibiting degeneration of a neuronal cell; (3)  
CC inhibiting formation of an ABP fibril on a cell; (4) inhibiting  
CC extracellular assembly of an ABP into a fibril; (5) inhibiting  
CC aggregation of ABP on the surface of a cell; (6) inhibiting infiltration  
CC of a microglial cell into senile plaques; (7) inhibiting activation of a

CC microglial cell by an ABP; (8) treating a subject with a condition  
CC associated with an interaction of an ABP with a receptor for RAGE on a  
CC cell; (9) evaluating the ability of an agent to inhibit binding of an  
CC ABP with a V-domain of a receptor for RAGE on the surface of a cell; (10)  
CC inhibiting activation of a NF-kappaB gene in a cell; (11) inhibiting  
CC periodontal disease in a subject; (12) inhibiting an RAGE's interaction  
CC with a receptor for RAGE when the receptor is on the surface of a cell;  
CC and (13) treating a subject with a condition associated with an  
CC interaction of an RAGE with a receptor for RAGE on a cell. The methods  
CC can be used for treating conditions associated with an interaction of an  
CC ABP or an RAGE with a receptor for RAGE, e.g. diabetes, Alzheimer's  
CC disease, senility, renal failure, hyperlipidaemic atherosclerosis,  
CC neuronal cytotoxicity, Down's syndrome, dementia associated with head  
CC trauma, amyotrophic lateral sclerosis, multiple sclerosis, amyloidosis,  
CC an autoimmune disease, inflammation, a tumour, cancer, male impotence,  
CC wound healing, periodontal disease, neuropathy, retinopathy, nephropathy  
CC or neuronal degeneration.

CC Sequence 30 AA:

QY Query Match 43.3%; Score 13; DB 20; Length 30;  
Best Local Similarity 100.0%; Pred. No. 7.7e-07;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QONTARIGEPLVL 14  
Db 2 qntarigeplvl 14

#### RESULT 14

AAV09351  
ID AAV09351 standard; peptide: 30 AA.

AC AAY09351;

DT 09-JUL-1999 (first entry)

DE Rat RAGE V-domain peptide SEQ ID NO:3.

XX RAGE: V-domain; receptor for advanced glycation endproduct;  
XX ligand binding site; amyloid-beta; Alzheimer's disease; Down's syndrome;  
XX senility; renal failure; hyperlipidaemic atherosclerosis; dementia;  
XX neuronal cytotoxicity; head trauma; amyotrophic lateral sclerosis;  
XX multiple sclerosis; amyloidosis; autoimmune disease; inflammation;  
XX tumour; cancer; male impotence; wound healing; periodontal disease;  
XX neuropathy; retinopathy; nephropathy; neuronal degeneration.

OS Rattus sp.

PN WO9918987-A1.

PD 22-APR-1999.

PF 09-OCT-1998; 98WO-US21346.

PR 09-OCT-1997; 97US-0948131.

PA (UYCO ) UNIV COLUMBIA NEW YORK.

PI Lamster I, Schmidt AM, Stern D, Yan SD;

DR WPI: 1999-277439/23.

XX New peptides based on an advanced glycation end product receptor are  
PT useful for treating Alzheimer's disease and Down's syndrome

PS Claim 4; Page 78; 101pp; English.

CC The present invention describes novel isolated peptides (1) having an  
CC amino acid sequence corresponding to an amino acid sequence of a  
CC V-domain of a receptor for an advanced glycation end product (RAGE).  
CC Also described are methods for: (1) inhibiting an amyloid-beta peptide

CC (ABP) interaction with a receptor for RAGE when the receptor is on the  
 CC surface of a cell; (2) inhibiting degeneration of a neuronal cell; (3)  
 CC inhibiting formation of an ABP fibril on a cell; (4) inhibiting  
 CC extracellular assembly of an ABP into a fibril; (5) inhibiting  
 CC aggregation of ABP on the surface of a cell; (6) inhibiting infiltration  
 CC of a microglial cell into senile plaques; (7) inhibiting activation of a  
 CC microglial cell by an ABP; (8) treating a subject with a condition  
 CC associated with an interaction of an ABP with a receptor for RAGE on a  
 CC cell; (9) evaluating the ability of an agent to inhibit binding of an  
 CC ABP with a V-domain of a receptor for RAGE on the surface of a cell; (10)  
 CC inhibiting activation of a NF-kappaB gene in a cell; (11) inhibiting  
 CC periodontal disease in a subject; (12) inhibiting an RAGE's interaction  
 CC with a receptor for RAGE when the receptor is on the surface of a cell;  
 CC and (13) treating a subject with a condition associated with an  
 CC interaction of an RAGE with a receptor for RAGE on a cell. The methods  
 CC can be used for treating conditions associated with an interaction of an  
 CC ABP or an RAGE with a receptor for RAGE, e.g. diabetes, Alzheimer's  
 CC disease, senility, renal failure, hyperlipidaemic atherosclerosis, a  
 CC neuronal cytotoxicity, Down's syndrome, dementia associated with head  
 CC trauma, amyotrophic lateral sclerosis, multiple sclerosis, amyloidosis,  
 CC an autoimmune disease, inflammation, a tumour, cancer, male impotence,  
 CC wound healing, periodontal disease, neuropathy, retinopathy, nephropathy  
 CC or neuronal degeneration.

SQ Sequence 30 AA;

Query Match 36.7%; Score 11; DB 20; Length 30;  
 Best Local Similarity 100.0%; Pred. No. 0.0001;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QNTTARIGEPL 12  
 |||||

Db 2 qnltarigepl 12

-RESULT 15

AAW44209 standard; peptide; 10 AA.

AC AAW44209;

DT 14-MAY-1998 (first entry)

DE Human soluble RAGE immunologically active fragment SEQ ID NO:13.

KW Human; soluble receptor; advanced glycosylation end product; RAGE;  
 KM AGE; antibody; vascular permeability; immunologically active fragment;  
 KW diabetes mellitus.

OS Homo sapiens.

XX WO9739125-A1.

PN 23-OCT-1997.

PD 11-APR-1997; 97WO-EP01834.

PR 16-APR-1996; 96US-0633148.

XX (SCHD ) SCHERING PATENTE AG.

PA Hollander DA, Morser MJ, Nagashima M;

XX WPI; 1997-558580/51.

DR Anti-advanced glycosylation end product polypeptide antibody -

XX prevents receptor binding and therefore reduces vascular

PT permeability, useful to treat diabetes mellitus

XX Claim 2; Page 47; 90pp; English.

CC The present sequence represents an immunologically active fragment

CC of a soluble human receptor to an advanced glycosylation end  
 CC product (RAGE) polypeptide. The present invention describes  
 CC an isolated antibody (Ab), specifically immunoreactive with  
 CC RAGE. Advanced glycosylation end products (AGE) of proteins are  
 CC non-enzymatically glycosylated proteins, which accumulate in vascular  
 CC tissue in ageing, and at an accelerated rate in individuals with  
 CC diabetes. The Ab, which prevents the interaction between an AGE and its  
 CC receptor (RAGE), reduces vascular permeability. The Ab can be used to  
 CC treat diabetes mellitus symptoms, e.g. microvasculopathy, occlusive  
 CC vascular disorders, neuropathy, nephropathy, retinopathy, haemodialysis  
 CC associated amyloidosis or atherosclerosis. The Ab can also be used for  
 CC the isolation and purification of human RAGE polypeptide.

SQ Sequence 10 AA;

Query Match 33.3%; Score 10; DB 18; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.0005;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 CKGAPKKRPQ 25  
 |||||

Db 1 ckgapkkrrpq 10

Search completed: July 31, 2002, 15:05:35  
 Job time: 110 sec



**This Page Blank (uspto)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 31, 2002, 15:03:45 ; Search time 14.58 seconds

(without alignments)  
197.715 Million cell updates/sec

Title: US-08-948-131-1

Perfect score: 30

Sequence: 1 AONITARIGEPLVLKCKGAPKPPQRLKWK 30

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 283138 seqs, 96089334 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

1: PIR-71:\*  
2: PIR1:\*  
3: PIR2:\*  
4: PIR3:\*  
5: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	30	100.0	404	1	161596 advanced glycosyla
2	13	43.3	402	2	T09062 probable advanced
3	10	33.3	416	1	A42879 advanced glycosyla
4	7	23.3	223	2	H64065 mutator muth - Hae
5	7	23.3	330	2	E81998 pseudouridylylate sy
6	7	23.3	330	2	H81225 ribosomal large ch
7	7	23.3	537	1	JQ1619 cell fusion glycop
8	7	23.3	594	2	AB3343 single-stranded-DN
9	7	23.3	595	2	B86212 protein F24B9.20 l
10	6	20.0	96	2	T07822 cysteine proteinase
11	6	20.0	110	2	S64538 hypothetical prote
12	6	20.0	155	2	T46154 hypothetical prote
13	6	20.0	159	2	D97739 30S ribosomal prot
14	6	20.0	201	2	A13484 low molecular weigh
15	6	20.0	204	2	A96024 probable acetyltra
16	6	20.0	209	2	E70536 hypothetical prote
17	6	20.0	230	2	A75260 hypothetical prote
18	6	20.0	234	1	Q0B443 membrane antigen g
19	6	20.0	238	2	H64181 ABC-type transport
20	6	20.0	242	2	AC2534 ABC-type prote
21	6	20.0	257	2	D70552 hypothetical prote
22	6	20.0	259	2	G86962 probable membrane
23	6	20.0	268	2	A12237 septum site-determ
24	6	20.0	269	2	AF3494 molycoprotein bios
25	6	20.0	271	2	A70415 molycoprotein bios
26	6	20.0	282	2	T07303 cell division inh
27	6	20.0	298	2	D87450 transcription regu
28	6	20.0	298	2	T51746 RNA helicase RH17
29	6	20.0	314	2	AH1912 hypothetical prote

30	6	20.0	326	2	H83187 hypothetical prote
31	6	20.0	333	2	AH1361 coat protein (Bact
32	6	20.0	334	2	D83164 conserved hypotet
33	6	20.0	336	2	B98209 hypothetical prote
34	6	20.0	336	2	AG3077 hypothetical prote
35	6	20.0	359	2	T35179 oxidoreductase alp
36	6	20.0	377	2	D97102 uncharacterized pr
37	6	20.0	387	2	C96670 hypothetical prote
38	6	20.0	389	2	S33667 probable integrase
39	6	20.0	429	2	T23984 hypothetical prote
40	6	20.0	435	2	AD2583 two component sens
41	6	20.0	468	2	H69133 argininosuccinate
42	6	20.0	471	2	S30585 hypothetical prote
43	6	20.0	474	2	B82227 exodeoxyribonuclea
44	6	20.0	479	2	C86275 hypothetical prote
45	6	20.0	481	2	S43687 serotonin receptor

#### ALIGNMENTS

RESULT 1  
161596 advanced glycosylation end-products receptor precursor - human  
N:Alternate names: advanced glycosylation end product-binding protein, 35K, glycoprotein  
C:Species: Homo sapiens (man)  
C>Date: 24-May-1996 #sequence, revision 07-Feb-1997 #text, change 16-Jul-1999  
C:Accession: 161596; B42879; S27968  
R:Sugaya, K.; Fukagawa, T.; Matsumoto, K.; Mita, K.; Takahashi, E.; Ando, A.; Inoko, G.  
Genomics 23, 408-419, 1994  
A:Title: Three genes in the human MHC class III region near the junction with the class II region of mouse mammary tumor gene int-3.  
A:Reference number: A55562; M01D:95137587  
A:Accession: 161596  
A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/  
A:Molecule type: DNA  
A:Residues: 1-404 <RES>  
A:Cross-references: GB:D28769; NID:9561657; PIDN:BA05958.1; PID:9561659  
R:Nepper, M.; Schmidt, A.M.; Brett, J.; Yan, S.D.; Wang, F.; Pan, Y.C.; Elliston, K.; J. Biol. Chem. 267, 14998-15004, 1992  
A:Title: Cloning and expression of a cell surface receptor for advanced glycosylation  
A:Reference number: A42879; M01D:92340547  
A:Accession: B42879  
A:Molecule type: mRNA  
A:Residues: 1-299, 'R', 101-404 <NE>  
A:Cross-references: EMBL:M91211; NID:9190845; PIDN:AA03574.1; PID:9190846  
A:Experimental source: lung  
A:Note: sequence extracted from NCBI backbone (NCBI:109438)  
C:Comment: Advanced glycosylation end products are heterogeneous nonenzymatically glycosylated cellular function, thus contributing to tissue lesions in diabetes.  
C:Comment: This receptor appears also to mediate the effects of amyloid beta peptide at the neurotoxic pathway that produces dementia in Alzheimer's disease.  
C:Genetics:  
A:Gene: GDB:AGER  
A:Cross-references: GDB:306354; OMIM:600214  
A:Map position: 6p21.3-6p21.3  
A:Intons: 18/1; 53/3; 119/1; 140/3; 170/1; 231/1; 274/3; 322/1; 331/1; 373/2  
C:Function:  
A:Description: neuronal receptor for amphoterin, a DNA-binding protein involved in neuronal glycosylation and products receptor; immunoglobulin homology  
C:Superfamily: Alzheimer's disease, glycoprotein, receptor; transmembrane protein  
C:Keywords: Alzheimer's disease, glycoprotein, receptor; transmembrane protein  
F:1-22/Domain: signal sequence #status predicted <SIG>  
F:23-404/Product: advanced glycosylation end products receptor; immunoglobulin homology  
F:23-404/Domain: extracellular #status predicted <EXT>  
F:31-101/Domain: immunoglobulin homology <IM1>  
F:137-210/Domain: immunoglobulin homology <IM2>  
F:252-303/Domain: immunoglobulin homology <IM3>  
F:345-362/Domain: transmembrane #status predicted <TM>  
F:363-404/Domain: intracellular #status predicted <INT>  
F:25/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:38-99, 144-208, 259-301/Disulfide bonds: #status predicted

Query Match 100.0%; Score 30; DB 1; Length 404;  
Best Local Similarity 100.0%; Pred. No. 2.1e-23;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONTARIGEPVLKCKGAPKPPORLEWK 30  
Db 23 AONTARIGEPVLKCKGAPKPPORLEWK 52

RESULT 2  
T09062  
probable advanced glycosylation end-products receptor precursor - mouse  
N:Alternate names: RAGE  
C:Species: Mus musculus (house mouse)  
C>Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 21-Jan-2000  
C:Accession: T09062  
R:Rowen, L.; Mahairas, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Loretz, C.; SC  
submitted to the EMBL Data Library, October 1997  
A:Description: Sequence of the mouse major histocompatibility locus class III region.  
A:Reference number: 216543  
A:Accession: T09062  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-402 <ROW>  
A:Cross-references: EMBL:AF030001; NID:g2564945; PID:g2564950  
C:Genetics:  
A:Gene: RAGE  
A:Map position: 17  
A:Insertions: 18/1; 53/3; 118/1; 139/3; 169/1; 229/1; 272/3; 320/1; 328/1; 371/2  
C:Superfamily: advanced glycosylation end products receptor; immunoglobulin homology  
C:Keywords: receptor; transmembrane protein  
F:31-100/Domain: immunoglobulin homology <IMM>

Query Match 43.3%; Score 13; DB 2; Length 402;  
Best Local Similarity 100.0%; Pred. No. 6.7e-06;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 QNTARIGEPLVL 14  
Db 24 QNTARIGEPLVL 36

RESULT 3  
A42879  
advanced glycosylation end-products receptor precursor - bovine  
N:Alternate names: advanced glycosylation end product-binding protein, 35k, glycoprotein  
C:Species: Bos primigenius taurus (cattle)  
C>Date: 04-Mar-1993 #sequence\_revision 07-Feb-1997 #text\_change 16-Jul-1999  
C:Accession: A42879; A42878; S27949  
R:Nepper, M.; Schmidt, A.M.; Bretz, J.; Yan, S.D.; Wang, F.; Pan, Y.C.; Elliston, K.; St  
J. Biol. Chem. 267, 14998-15004, 1992  
A:Title: Cloning and expression of a cell surface receptor for advanced glycosylation en  
A:Reference number: A42879; MUID:92340547  
A:Accession: A42879  
A:Molecule type: mRNA  
A:Residues: 1-416 <NE>  
A:Cross-references: GB:M91212; NID:g163650; PIDN:AAA03575.1; PID:g163651  
A:Experimental source: lung  
A:Note: sequence extracted from NCBI backbone (NCBI:P:109436)  
A:Note: parts of this sequence, including the amino end of the mature protein, were dete  
R:Schmidt, A.M.; Viana, M.; Gerlich, M.; Bretz, J.; Ryan, J.; Kao, J.; Esposito, C.; He  
J. Biol. Chem. 267, 14987-14997, 1992  
A:Title: Isolation and characterization of two binding proteins for advanced glycosylati  
A:Reference number: A42878; MUID:92340546  
A:Accession: A42878  
A:Molecule type: protein  
A:Residues: 23-24, 'X', 26-37, 'X', 39-49, 'XX', 52-54 <SCH>  
A:Experimental source: endothelial cells  
A:Note: sequence extracted from NCBI backbone (NCBI:P:109434)  
C:Comment: Advanced glycosylation end products are heterogeneous nonenzymatically glycos  
cellular function, thus contributing to tissue lesions in diabetes.  
C:Comment: This receptor appears also to mediate the effects of amyloid beta peptide on

ates in the neurotoxic pathway that produces dementia in Alzheimer's disease.  
A:Function:  
C:Description: neuronal receptor for amphoterin, a DNA-binding protein involved in ne  
C:Superfamily: advanced glycosylation end products receptor; immunoglobulin homology  
C:Keywords: Alzheimer's disease; glycoprotein; receptor; transmembrane protein  
F:1-32/Domain: signal sequence #status predicted <SIG>  
F:23-416/Product: advanced glycosylation end-products receptor RAGE #status predicted  
F:23-354/Domain: extracellular #status predicted <EXT>  
F:31-100/Domain: immunoglobulin homology <IM1>  
F:136-209/Domain: immunoglobulin homology <IM2>  
F:262-313/Domain: immunoglobulin homology <IM3>  
F:353-372/Domain: transmembrane #status predicted <TM>  
F:373-416/Domain: intracellular #status predicted <INT>  
F:25,80/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:38-98,143-207,269-311/Disulfide bonds: #status predicted

Query Match 33.3%; Score 10; DB 1; Length 416;  
Best Local Similarity 100.0%; Pred. No. 0.0084;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 CKGAPKPPQ 25  
Db 38 CKGAPKPPQ 47

RESULT 4  
H64065  
mutator mutn - Haemophilus influenzae (strain Rd KW20)  
N:Alternate names: DNA mismatch protein  
C:Species: Haemophilus influenzae  
C>Date: 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 26-Aug-1999  
C:Accession: H64065  
R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage  
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman  
, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M.  
Science 269, 496-512, 1995  
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente  
A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.  
A:Reference number: A64000; MUID:95350630  
A:Accession: H64065  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-223 <TRIG>  
A:Cross-references: GB:U32723; GB:L42023; NID:g1573363; PIDN:AC22062.1; PID:g1573374  
C:Genetics:  
A:Gene: mutn  
C:Superfamily: mutator mutn

Query Match 23.3%; Score 7; DB 2; Length 223;  
Best Local Similarity 100.0%; Pred. No. 6.3;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 ITARIGE 10  
Db 165 ITARIGE 171

RESULT 5  
E81998  
pseudouridylate synthase (EC 4.2.1.70) C rRNA-specific NMA0070 [imported] - Neisseria  
C:Species: Neisseria meningitidis  
C>Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 02-Feb-2001  
C:Accession: E81998  
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mo  
; Holtroyd, S.; Jagers, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajand  
Nature 404, 502-506, 2000  
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491  
A:Reference number: A81775; MUID:20222556  
A:Accession: E81998  
A:Status: preliminary  
A:Molecule type: DNA

A:Residues: 1-330 <PAR>  
A:Cross-references: GB:AL162752; GB:AL157959; NID:g7378778; PIDN:CAB83386.1; PID:g737884  
A:Experimental source: serogroup A, strain Z2491  
C:Genetics:  
A:Gene:rluc; NMA0070  
C:Superfamily: conserved hypothetical protein HI0176  
C:Keywords: carbon-oxygen lyase; hydro-lyase

Query Match 23.3%; Score 7; DB 2; Length 330;  
Best Local Similarity 100.0%; Pred. No. 8.6;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 GEPLVTK 15  
Db 304 GEPLVTK 310

RESULT 6

H81225  
ribosomal large chain pseudouridine synthase C NMB0198 [imported] - Neisseria meningitidis  
C:Species: Neisseria meningitidis  
C>Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 19-Jan-2001  
C:Accession: H81225

R:Retellin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.  
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;  
rt, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignanl, V.; Pizza, M.  
Science 287, 1809-1815, 2000  
A:Authors: Grandt, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappoli, R.; V  
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.  
A:Reference number: AB1000; MUID:20175755  
A:Accession: H81225

A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-330 <DET>  
A:Cross-references: GB:AE002377; GB:AE002098; NID:g7225416; PIDN:AAF40655.1; PID:g722541  
A:Experimental source: serogroup B, strain MC58  
C:Genetics:  
A:Gene: NMB0198  
C:Superfamily: conserved hypothetical protein HI0176

Query Match 23.3%; Score 7; DB 2; Length 330;  
Best Local Similarity 100.0%; Pred. No. 8.6;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 GEPLVTK 15  
Db 304 GEPLVTK 310

RESULT 7

JQ1619  
cell fusion glycoprotein precursor - pneumonia virus of mice  
N:Alternate names: F protein  
N:Contains: cell fusion glycoprotein F1; cell fusion glycoprotein F2

C:Species: pneumonia virus of mice  
C>Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 25-Oct-1996  
C:Accession: JQ1619  
R:Chambers, P.; Pringle, C.R.; Easton, A.J.  
J. Gen. Virol. 73, 1717-1724, 1992  
A:Title: Sequence analysis of the gene encoding the fusion glycoprotein of pneumonia vi  
A:Reference number: JQ1619; MUID:92333256  
A:Accession: JQ1619  
A:Molecule type: mRNA  
A:Residues: 1-537 <CH>  
A:Cross-references: GB:S40186  
C:Genetics:  
A:Gene: F

C:Superfamily: cell fusion glycoprotein  
C:Keywords: glycoprotein; membrane fusion; transmembrane protein  
F:1-22/Domain: signal sequence #status predicted <SIG>  
F:23-101/Product: cell fusion glycoprotein F2 #status predicted <FG2>

F:102-537/Product: cell fusion glycoprotein F1 #status predicted <FG1>  
F:491-514/Domain: transmembrane #status predicted <TM>  
F:463,488/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 23.3%; Score 7; DB 1; Length 537;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 GEPLVTK 15  
Db 434 GEPLVTK 440

RESULT 8

AB3343  
single-stranded-DNA-specific exonuclease recJ (EC 3.1.-.-) [imported] - Brucella meli  
C:Species: Brucella melitensis  
C>Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 15-Feb-2002

C:Accession: AB3343  
R:DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mijer, C.; Los, T.; Ivanov  
.; Mazur, M.; Goldsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Let  
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002  
A:Title: The genome sequence of the facultative intracellular pathogen Brucella meli

A:Reference number: AD3252; PMID:11756688  
A:Accession: AB3343  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-594 <KUR>  
A:Cross-references: GB:AE008917; PIDN:AM151909.1; PID:g17982663; GSPDB:GN00190  
A:Experimental source: strain 16M  
C:Genetics:  
A:Gene: BMEI0728  
A:Map position: 1  
C:Superfamily: single-stranded-DNA-specific exonuclease RecJ

Query Match 23.3%; Score 7; DB 2; Length 594;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 ARIGEPL 12  
Db 287 ARIGEPL 293

RESULT 9

B86212  
protein F24B9.20 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C>Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001  
C:Accession: B86212  
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,  
ansen, N.F.; Hughes, B.; Hlizar, L.  
Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maitl, R.; Marzia  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: A86141; MUID:210167719  
A:Accession: B86212  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-595 <STO>  
A:Cross-references: GB:AE005172; NID:g8439898; PIDN:AAF75084.1; GSPDB:GN00141

C:Genetics:  
A:Gene: F24B9.20  
A:Map position: 1

Query Match 23.3%; Score 7; DB 2; Length 595;  
 Best Local Similarity 100.0%; Pred. No. 14;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 RIGEPV 13  
 |||||  
 Db 550 RIGEPV 556

RESULT 10  
 T07822  
 cystein proteinase inhibitor - cucumber  
 C:Species: Cucumis sativus (cucumber)  
 C:Date: 14-May-1999 #sequence\_revision 14-May-1999 #text\_change 20-Jun-2000  
 C:Accession: T07822  
 R:Yamakawa, S.  
 submitted to the EMBL Data Library, May 1998  
 A:Description: Cystein proteinase inhibitor.  
 A:Reference number: Z16154  
 A:Accession: T07822  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-96 <YAM>  
 A:Cross-references: EMBL:AB014760; PIDN:BA28867.1  
 A:Note: root-specific  
 C:Superfamily: cystatin; cystatin homology  
 C:Keywords: cysteine proteinase inhibitor

Query Match 20.0%; Score 6; DB 2; Length 96;  
 Best Local Similarity 100.0%; Pred. No. 34;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LVLCK 17  
 |||||  
 Db 59 LVLCK 64

RESULT 11  
 S64538  
 hypothetical protein YGR215w - yeast (Saccharomyces cerevisiae)  
 N:Alternate names: hypothetical protein G7821  
 C:Species: Saccharomyces cerevisiae  
 C:Date: 17-May-1996 #sequence\_revision 17-May-1996 #text\_change 20-Jun-2000  
 R:Rieger, M.; Mueller-Auer, S.; Brueckner, M.; Schaefer, M.  
 submitted to the Protein Sequence Database, May 1996  
 A:Reference number: S64071  
 A:Accession: S64538  
 A:Molecule type: DNA  
 A:Residues: 1-110 <RIE>  
 A:Cross-references: EMBL:Z73000; NID:G1323386; PID:G1323387; GSPDB:GN00007; MIPS:YGR215A  
 A:Experimental source: strain S288C  
 C:Genetics:  
 A:Gene: MIPS:YGR215W  
 A:Map position: 7R  
 C:Superfamily: Saccharomyces cerevisiae hypothetical protein YGR215w

Query Match 20.0%; Score 6; DB 2; Length 110;  
 Best Local Similarity 100.0%; Pred. No. 38;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 17 KGAPK 22  
 |||||  
 Db 88 KGAPK 93

RESULT 12  
 T46154  
 hypothetical protein T4D2.10 - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 04-Feb-2000 #sequence\_revision 04-Feb-2000 #text\_change 04-Feb-2000

C:Accession: T46154  
 R:Nyakatura, G.; Fartmann, B.; Dauner, D.; Sterr, W.; Holland, R.; Weichselgartner, M.  
 submitted to the Protein Sequence Database, December 1999  
 A:Reference number: Z23025  
 A:Accession: T46154  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-155 <NYA>  
 A:Cross-references: EMBL:AL132958  
 A:Experimental source: cultivar Columbia; BAC clone T4D2  
 C:Genetics:  
 A:Map position: 3  
 A:Introns: 118/3  
 A:Note: T4D2.10

Query Match 20.0%; Score 6; DB 2; Length 155;  
 Best Local Similarity 100.0%; Pred. No. 50;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 KCKGAP 20  
 |||||  
 Db 139 KCKGAP 144

RESULT 13  
 D97739  
 30S ribosomal protein S9 [Imported] - Rickettsia conorii (strain Malish 7)  
 C:Species: Rickettsia conorii  
 C:Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 30-Sep-2001  
 C:Accession: D97739  
 R:Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.;  
 Science 293, 2093-2098, 2001  
 A:Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.  
 A:Reference number: A97700; MUID:21442074; PMID:11557893  
 A:Accession: D97739  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-159 <KUR>  
 A:Cross-references: GB:AE006914; PIDN:AL02854.1; PID:G15619376; GSPDB:GN00173  
 C:Genetics:  
 A:Gene: rps1

Query Match 20.0%; Score 6; DB 2; Length 159;  
 Best Local Similarity 100.0%; Pred. No. 51;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EPLVVK 15  
 |||||  
 Db 18 EPLVVK 23

RESULT 14  
 A13484  
 low molecular weight phosphotyrosine protein phosphatase (EC 3.1.3.48) [Imported] - B  
 C:Species: Brucella melitensis  
 C:Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 01-Feb-2002  
 C:Accession: A13484  
 R:DeLavecchio, V.G.; Kaptrai, V.; Redkar, R.J.; Patra, G.; Mijer, C.; Los, T.; Ivanov  
 Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002  
 A:Title: The genome sequence of the facultative intracellular pathogen Brucella melit  
 A:Reference number: AD3252; PMID:11756688  
 A:Accession: A13484  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-201 <KUR>  
 A:Cross-references: GB:AE008917; PIDN:AL53044.1; PID:G17983904; GSPDB:GN00190  
 A:Experimental source: strain 16M  
 C:Genetics:  
 A:Gene: BMEI163  
 A:Map position: I



C:Keywords: phosphoric monoester hydrolase

Query Match 20.0%; Score 6; DB 2; Length 201;  
 Best Local Similarity 100.0%; Pred. No. 62;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 ITARIG 9  
 |||||  
 DB 140 ITARIG 145

# RESULT 15

A96024  
 Probable acetyltransferase protein (EC 2.3.1.-) [Imported] - Sinorhizobium meliloti (str C);Species: Sinorhizobium meliloti  
 C:Date: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_change 30-Sep-2001  
 C:Accession: A96024  
 R:Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001  
 A:Title: The complete sequence of the 1,683-kb PSymb megaplasmid from the N2-fixing endo A:Reference number: A95842; MUID:21396508; PMID:11481431  
 A:Accession: A96024  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-204 <KUR>  
 A:Cross-references: GB:AL591985; PIDN:CAC49857.1; PID:q15141345; GSPDB:GN00167  
 A:Experimental source: strain 1021, megaplasmid PSymb  
 R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, P.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; L.: Hyman, R.W.; Jones, T. Science 293, 668-672, 2001  
 A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, Hebut, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K. A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.  
 A:Reference number: A96039; MUID:21368234; PMID:11474104  
 A:Contents: annotation  
 C:Genetics:  
 A:Gene: SMD20765  
 A:Genome: Plasmid  
 C:Superfamily: Agrobacterium chloramphenicol acetyltransferase  
 C:Keywords: acyltransferase

Query Match 20.0%; Score 6; DB 2; Length 204;  
 Best Local Similarity 100.0%; Pred. No. 63;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 TARIGE 10  
 |||||  
 DB 164 TARIGE 169

Search completed: July 31, 2002, 15:04:30  
 Job time: 45 sec

This Page Blank (uspto)

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 31, 2002, 15:04:35 ; Search time 10.35 Seconds

(without alignments)  
112.231 Million cell updates/sec

Title: US-08-948-131-1

Perfect score: 30  
Sequence: 1 AONTARAGEPLVLCRCGAPKKPQRLMK 30

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 105224 seqs, 38719550 residues

Word size : 0

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	404	1 RAGE_HUMAN	Q15109 homo sapien
2	13	43.3	403	1 RAGE_MOUSE	Q62151 mus musculu
3	11	36.7	402	1 RAGE_RAT	Q63495 rattus norv
4	10	33.3	416	1 RAGE_BOVIN	Q28173 bos taurus
5	7	23.3	223	1 MUTH_HAEN	P44688 haemophilus
6	7	23.3	537	1 VGLF_PVN	P35949 pneumonia v
7	6	20.0	110	1 YG4L_YEAST	P53305 saccharomyc
8	6	20.0	159	1 RS9_RICCN	Q92144 rickettsia
9	6	20.0	181	1 YCF4_GUTTH	Q78467 guillardia
10	6	20.0	210	1 VA79_HAEN	P45073 haemophilus
11	6	20.0	234	1 VGP8_EBV	P03224 epstein-bar
12	6	20.0	259	1 E434_ADECT	P87368 canine aden
13	6	20.0	265	1 E434_ADECC	Q65962 canine adeq
14	6	20.0	265	1 E434_ADECR	Q96690 canine aden
15	6	20.0	269	1 MIND_GUTTH	C78436 guillardia
16	6	20.0	278	1 PROC_VIBAL	P52053 vibrio algi
17	6	20.0	282	1 MIND_CHIVU	P56346 chlorella v
18	6	20.0	401	1 ENO_THEC	Q9HJ11 thermoplasm
19	6	20.0	429	1 YRM4_CAEEL	Q09415 caenorhabd
20	6	20.0	468	1 ARLY_MERTH	Q26369 methanobact
21	6	20.0	481	1 SH2B_HUMAN	P41595 homo sapien
22	6	20.0	482	1 DUSA_HUMAN	Q9Y666 homo sapien
23	6	20.0	504	1 SH2B_MOUSE	Q02152 mus musculu
24	6	20.0	513	1 SPT1_HUMAN	Q43278 homo sapien
25	6	20.0	607	1 UVRC_PSEFL	P32966 pseudomonas
26	6	20.0	626	1 RN17_MOUSE	Q99M77 mus musculu
27	6	20.0	635	1 SYT_RICPR	Q05947 rickettsia
28	6	20.0	714	1 EFG_MYCTU	Q07170 mycobacteri
29	6	20.0	754	1 ASPH_BOVIN	Q28056 bos taurus
30	6	20.0	757	1 ASPH_HUMAN	Q12757 homo sapien
31	6	20.0	788	1 REC2_HAEN	P44408 haemophilus
32	6	20.0	837	1 HFC1_HAEN	P33397 haemophilus
33	6	20.0	837	1 HFC2_HAEN	P45997 haemophilus

#### ALIGNMENTS

```

RESULT 1
ID RAGE_HUMAN STANDARD; PRT; 404 AA.
AC Q15109; Q15279; Q9Y3R3; Q9H2X7;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Advanced glycosylation end product-specific receptor precursor
DE (receptor for advanced glycosylation end products).
GN ASGR OR RAGE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Lung;
RX MEDLINE=92340547; PubMed=1378843;
RA Neepor M., Schmidt A.M., Brett J., Yan S.D., Wang F., Pan Y.C.,
RA Elliston K., Stern D., Shaw A.;
RT "Cloning and expression of a cell surface receptor for advanced
RT glycosylation end products of proteins.";
RL J. Biol. Chem. 267:14998-15004(1992).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=95137587; PubMed=7835890;
RA Sugaya K., Fukagawa T., Matsumoto K., Mita K., Takahashi E., Ando A.,
RA Inoko H., Ikemura T.;
RT "Three genes in the human MHC class III region near the junction with
RT the class II: gene for receptor of advanced glycosylation end
RT products, PBX2 homeobox gene and a notch homolog, human counterpart
RT of mouse mammary tumor gene Int-3.";
RL Genomics 23:408-419(1994).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Rowen L., Dankers C., Baskin D., Faust J., Loretz C., Ahearn M.E.,
RA Banta A., Spies T., Hood L.;
RT Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANT ARG-100.
RA Acedin M.J., Yonekura H., Migita H., Karasawa J., Yamamoto Y.,
RA Yamamoto H.;
RT "Molecular heterogeneity of the receptor for advanced glycation
RT endproducts.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RA Melherbe P., Richards J., Gaillard H., Thompson A., Diener C.,
RA Schuller A., Huber G.;
RT "cDNA cloning of a novel secreted isoform of the human Receptor for
RT Advanced Glycation End products (RAGE) and characterization of cells
RT co-expressing cell-surface scavenger receptors and Swedish mutant
RT amyloid precursor protein.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE OF 1-12 FROM N.A.

```

RA	Hudson B.I., Futers T.S.;
RT	"Novel polymorphisms in the receptor for advanced glycation end-products (RAGE) gene".
RL	Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC	-1- FUNCTION: MEDIATES INTERACTIONS OF ADVANCED GLYCOSYLATION END PRODUCTS (AGE). THESE ARE NONENZYMATICALLY GLYCOSYLATED PROTEINS WHICH ACCUMULATE IN VASCULAR TISSUE IN AGING AND AT AN ACCELERATED RATE IN DIABETES.
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (ISOFORM 1) AND SECRETED (ISOFORM 2).
CC	-1- ALTERNATIVE PRODUCTS: 2 ISOFORMS, 1 (SHOWN HERE) AND 2/RAGESEC; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC	-1- TISSUE SPECIFICITY: ENDOTHELIAL CELLS.
CC	-1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC	-1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
CC	-1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <a href="http://www.isb-sib.ch/announce/or_send_an_email_to_license@isb-sib.ch">http://www.isb-sib.ch/announce/or_send_an_email_to_license@isb-sib.ch</a> ).
CC	-----
DR	EMBL; M91211; AAA03574.1; -
DR	EMBL; D28769; BAA05958.1; -
DR	EMBL; U89336; AAB47491.1; -
DR	EMBL; AB036432; BAA83369.1; -
DR	EMBL; AJ133822; CAB83108.1; -
DR	EMBL; AF208289; AAG35728.1; -
DR	MIM; 600214; -
DR	InterPro: IPRO031006; IG_MHC.
DR	InterPro: IPRO03598; IG_c2.
DR	InterPro: IPRO03600; IG_1like.
DR	Pfam; PF00047; Ig_2.
DR	SMART; SM00410; IG_1like; 1.
DR	SMART; SM00408; IGC2; 1.
DR	PROSITE; PS00290; IG_MHC; 1.
KW	Immunoglobulin domain; Glycoprotein; Transmembrane; Repeat; signal; Alternative splicing; Polymorphism.
KW	SIGNAL
FT	CHAIN
FT	23 404
FT	22
FT	POTENTIAL.
FT	ADVANCED GLYCOSYLATION END PRODUCT-SPECIFIC RECEPTOR.
FT	EXTRACELLULAR (POTENTIAL).
FT	CYTOLASMIC (POTENTIAL).
FT	IG-LIKE V-TYPE DOMAIN.
FT	IG-LIKE C2-TYPE DOMAIN.
FT	IG-LIKE C2-TYPE DOMAIN 2.
FT	POTENTIAL.
FT	POTENTIAL.
FT	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	POLY-GU.
FT	MISSING (IN ISOFORM 2).
FT	GVPLEPSPVLIIIPGSDPDQATGYSCVAATHSSGPOESRA VISITIEEGEGEPNAGSGGSLGTLLALVLTGGLTGAL LIGVILWQRQRKEERRAPENOEERAEALNSEEPKESSTGGP -> VSDLERAGATRRGANCRLCGIRIAGNS PGPDGPGRPGDSRAHMGHLVAKAATPRGREGPRKPCGRC GACRESEVGCT (IN ISOFORM 2).
FT	O -> R.
FT	/FTId-VAR_011338.
FT	M -> G (IN REF. 1).
FT	SEQUENCE
SO	CONFLECT 1 1
SO	404 AA; 42802 MM; 0D584C436C30CCE7 CRC64;
Query Match	100.0%; Score 30; DB 1; Length 404;
Best Local Similarity	100.0%; Prid. No. 4.Be-25;
Matches 30; Conservative	0; Mismatches 0; Indels 0; Gaps 0;

QY	1	QONTARIGEPLVLCCKGAPKKPPORLEMK	30
DB	23	QONTARIGEPLVLCCKGAPKKPPORLEMK	52
RESULT	2		
ID	RAGE_MOUSE	STANDARD:	PRT: 403 AA.
AC	062151:		
DT	01-NOV-1997 (Rel. 35, Created)		
DT	01-NOV-1997 (Rel. 35, Last sequence update)		
DT	01-MAR-2002 (Rel. 41, Last annotation update)		
DE	Advanced glycosylation and product-specific receptor precursor		
DE	(Receptor for advanced glycosylation and products).		
GN	AGER OR RAGE.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxId:10090;		
RP	(1)		
RC	SEQUENCE FROM N.A.		
RC	STRAIN-BALB/C; TISSUE=Lung;		
RX	MEDLINE=97368045; PubMed=97224812;		
RA	Renard C., Chappey O., Wautler M.P., Nagashima M., Lunn E.,		
RA	Morser J., Zhao L., Schmidt A.M., Scherrmann J.M., Wautler J.L.;		
RT	"Recombinant advanced glycation and product receptor pharmacokinetics		
RT	in normal and diabetic rats.";		
RL	Mol. Pharmacol. 52:54-62(1997).		
CC	-1- FUNCTION: MEDIATES INTERACTIONS OF ADVANCED GLYCOSYLATION END		
CC	PRODUCTS (AGE). THESE ARE NONENZYMATICALLY GLYCOSYLATED PROTEINS		
CC	WHICH ACCUMULATE IN VASCULAR TISSUE IN AGING AND AT AN ACCELERATED		
CC	RATE IN DIABETES.		
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.		
CC	-1- TISSUE SPECIFICITY: ENDOTHELIAL CELLS.		
CC	-1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.		
CC	-1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.		
CC	-1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C-TYPE DOMAINS.		
CC	-----		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration		
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -		
CC	the European Bioinformatics Institute. There are no restrictions on its		
CC	use by non-profit institutions as long as its content is in no way		
CC	modified and this statement is not removed. Usage by and for commercial		
CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>		
CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).		
CC	-----		
DR	EMBL; L3412; AAA40040.1; -.		
DR	MGI; MGI:893592; Ager.		
DR	InterPro: IPR003006; IG_MHC.		
DR	InterPro: IPR003598; IG_C2.		
DR	InterPro: IPR003600; IG_Like.		
DR	Pfam; PF00047; Ig; 3.		
DR	SMART; SM00410; IG_Like; 1.		
DR	SMART; SM00408; IGC2; 1.		
DR	PROSITE; PS00290; IG_MHC; 1.		
KW	Immunoglobulin domain; Glycoprotein; Transmembrane; Repeat; Signal.		
FT	SIGNAL	1	22
FT	CHAIN	23	403
FT	POTENTIAL.		
FT	ADVANCED GLYCOSYLATION END PRODUCT-		
FT	SPECIFIC RECEPTOR.		
FT	EXTRACELLULAR (POTENTIAL).		
FT	POTENTIAL.		
FT	CYTOPLASMIC (POTENTIAL).		
FT	IG-LIKE V-TYPE DOMAIN.		
FT	IG-LIKE C2-TYPE DOMAIN 1.		
FT	IG-LIKE C2-TYPE DOMAIN 2.		
FT	POTENTIAL.		
FT	POTENTIAL.		
FT	POTENTIAL.		
FT	N-LINKED (GLCNAC. . .) (POTENTIAL).		
FT	N-LINKED (GLCNAC. . .) (POTENTIAL).		
FT	CARBOHYD	80	80
FT	CARBOHYD	80	80
FT	SEQUENCE	403 AA;	42668 MW;
FT			1279796FD1579357 CRC64;

Query Match 43.3%; Score 13; DB 1; Length 403;

Best Local Similarity 100.0%; Pred. No. 9e-07; Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 QNTARIGEPLV 14  
Db 24 QNTARIGEPLV 36

```

RESULT 3
RAGE_RAT ID RAGE_RAT STANDARD: PRT: 402 AA.
AC 063495;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Advanced glycosylation end product-specific receptor precursor
DE (Receptor for advanced glycosylation end products).
GN AGER OR RAGE.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Lung;
RX MEDLINE=97368045; Pubmed=9224812;
RA Renard C., Chappey O., Wautier M.P., Nagashima M., Lunn E.,
RA Moser J., Zhao L., Schmidt A.M., Schermann J.M., Wautier J.L.;
RT Recombinant advanced glycation end product receptor pharmacokinetics
RT in normal and diabetic rats.
RT Mol. Pharmacol. 52:54-62(1997).
CC -1- FUNCTION: MEDIATES INTERACTIONS OF ADVANCED GLYCOSYLATION END
CC PRODUCTS (AGE). THESE ARE NONENZYMATICALLY GLYCOSYLATED PROTEINS
CC WHICH ACCUMULATE IN VASCULAR TISSUE IN AGING AND AT AN ACCELERATED
CC RATE IN DIABETES.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: ENDOTHELIAL CELLS.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: L33413; AAA42027.1; -
CC InterPro: IPR003006; Ig_MHC.
CC InterPro: IPR003598; Ig_C2.
CC InterPro: IPR003600; Ig_Like.
CC Pfam: PF00047; Ig_3.
CC SMART: SM00410; Ig_Like; 1.
CC SMART: SM00408; IGC2; 1.
CC PROSITE: PS00290; Ig_MHC; 1.
CC Immunoglobulin domain; Glycoprotein; Transmembrane; Repeat; Signal.
CC SIGNAL 1 22
CC CHAIN 23 402
CC ADVANCED GLYCOSYLATION END PRODUCT-
CC SPECIFIC RECEPTOR.
CC EXTRACELLULAR (POTENTIAL).
CC POTENTIAL.
CC CYTOPLASMIC (POTENTIAL).
CC IG-LIKE V-TYPE DOMAIN.
CC IG-LIKE C2-TYPE DOMAIN 1.
CC IG-LIKE C2-TYPE DOMAIN 2.
CC POTENTIAL.
CC DISULFID 38 98
CC DISULFID 143 206
CC DISULFID 257 299
CC CARBOHYD 25 25
CC CARBOHYD 80 80
CC N-LINKED (GLCNAC. . .) (POTENTIAL).
CC N-LINKED (GLCNAC. . .) (POTENTIAL).

```

SO SEQUENCE 402 AA; 42663 MW; 59448BC3A51E94E CRC64;

Query Match 36.7%; Score 11; DB 1; Length 402;

Best Local Similarity 100.0%; Pred. No. 0.00013; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 QNTARIGEPL 12  
Db 24 QNTARIGEPL 34

```

RESULT 4
RAGE_BOVIN ID RAGE_BOVIN STANDARD: PRT: 416 AA.
AC Q28173;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Advanced glycosylation end product-specific receptor precursor
DE (Receptor for advanced glycosylation end products).
GN AGER OR RAGE.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OC NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE=92340547; Pubmed=1378843;
RA Nepper M., Schmidt A.M., Brett J., Yan S.D., Wang F., Pan Y.C.,
RA Elliston K., Stern D., Shaw A.;
RT Cloning and expression of a cell surface receptor for advanced
RT glycosylation end products of proteins.
RT J. Biol. Chem. 267:14998-15004(1992).
CC -1- FUNCTION: MEDIATES INTERACTIONS OF ADVANCED GLYCOSYLATION END
CC PRODUCTS (AGE). THESE ARE NONENZYMATICALLY GLYCOSYLATED PROTEINS
CC WHICH ACCUMULATE IN VASCULAR TISSUE IN AGING AND AT AN ACCELERATED
CC RATE IN DIABETES.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: ENDOTHELIAL CELLS.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M91212; AAA3575.1; -
CC InterPro: IPR003006; Ig_MHC.
CC InterPro: IPR003598; Ig_C2.
CC InterPro: IPR003600; Ig_Like.
CC Pfam: PF00047; Ig_2.
CC SMART: SM00410; Ig_Like; 1.
CC SMART: SM00408; IGC2; 1.
CC PROSITE: PS00290; Ig_MHC; 1.
CC Immunoglobulin domain; Glycoprotein; Transmembrane; Repeat; Signal.
CC SIGNAL 1 22
CC CHAIN 23 416
CC ADVANCED GLYCOSYLATION END PRODUCT-
CC SPECIFIC RECEPTOR.
CC EXTRACELLULAR (POTENTIAL).
CC POTENTIAL.
CC CYTOPLASMIC (POTENTIAL).
CC IG-LIKE V-TYPE DOMAIN.
CC IG-LIKE C2-TYPE DOMAIN 1.
CC IG-LIKE C2-TYPE DOMAIN 2.
CC POTENTIAL.
CC DISULFID 38 98

```

FT DISULFID 143 207 POTENTIAL.  
 FT DISULFID 269 311 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 25 25 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 80 80 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT DOMAIN 391 396 POLY-GLU.  
 SQ SEQUENCE 416 AA; 44182 MW; B703815573E767AE CRC64;

Query Match 33.3%; Score 10; DB 1; Length 416;  
 Best Local Similarity 100.0%; Pred. No. 0.0016;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 CKGAPKRPQ 25  
 |||||||||  
 Db 38 CKGAPKRPQ 47

RESULT 5  
 MUTH\_HAETN  
 ID MUTH\_HAETN STANDARD; PRT; 223 AA.  
 AC P44688;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE DNA mismatch repair protein muth.  
 GN MUTH OR HI0403  
 OS Haemophilus influenzae.  
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;  
 CC Haemophilus.  
 OX NCBI\_Taxid=727;  
 RN 11  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-RD / KW20 / ATCC 51907;  
 RX MEDLINE=95350630; PubMed=7542800;  
 RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,  
 RA Kerevasage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,  
 RA McInerney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,  
 RA Scott J.D., Shetty R., Liu L.-I., Glodek A., Kelley J.M.,  
 RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,  
 RA Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,  
 RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghegan N.S.M.,  
 RA Gnehm C.V., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,  
 RA Venter J.C.;  
 RT "Whole-genome random sequencing and assembly of Haemophilus  
 RT influenzae Rd.";  
 RL Science 269:496-512(1995).  
 CC -1- FUNCTION: SEQUENCE-SPECIFIC ENDONUCLEASE THAT CLEAVES UNMETHYLATED  
 CC GATC SEQUENCES. IT IS INVOLVED IN DNA MISMATCH REPAIR (BY  
 CC SIMILARITY).  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 CC EMBL: U32723; AAC22062.1; -  
 DR HSSP: P06722; 2A2O.  
 DR TIGR: HI0403; -  
 DR InterPro: IPR004230; Muth.  
 DR Pfam: PF02976; Muth; 1.  
 KW DNA repair; Hydrolase; Endonuclease; Complete Proteome.  
 SQ SEQUENCE 223 AA; 24906 MW; 339A4E9DA0E622A CRC64;

Query Match 23.3%; Score 7; DB 1; Length 223;  
 Best Local Similarity 100.0%; Pred. No. 1.5;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 ITARIGE 10  
 |||||||

Db 165 ITARIGE 171

RESULT 6  
 VGLF\_PVM  
 ID VGLF\_PVM STANDARD; PRT; 537 AA.  
 AC P35949;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;  
 DE Fusion glycoprotein F1].  
 GN F.  
 OS Pneumonia virus of mice (PVM).  
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
 OC Paramyxoviridae; Pneumovirinae; Pneumovirus.  
 OX NCBI\_Taxid=11263;  
 RN 11  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92333256; PubMed=1629698;  
 RA Chambers P., Pringle C.R., Easton A.J.;  
 RT "Sequence analysis of the gene encoding the fusion glycoprotein of  
 RT pneumonia virus of mice suggests possible conserved secondary  
 RT structure elements in paramyxovirus fusion glycoproteins."  
 RL J. Gen. Virol. 73:1717-1724(1992).  
 CC -1- FUNCTION: THIS PROTEIN DIRECTS FUSION OF VIRAL AND CELLULAR  
 CC MEMBRANES, RESULTING IN VIRAL PENETRATION, & CAN DIRECT FUSION OF  
 CC INFECTED CELLS WITH ADJOINING CELLS, RESULTING IN THE FORMATION OF  
 CC SYNCYTIA.  
 CC -1- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2  
 CC LINKED BY A DISULFIDE BOND.  
 CC -1- SIMILARITY: BELONGS TO THE PARAMYXOVIRUSES FUSION GLYCOPROTEIN  
 CC FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 CC EMBL: D11128; BAA01902.1; -  
 DR PIR: JQ1619; JQ1619.  
 DR InterPro: IPR000776; Fusion\_gly.  
 DR Pfam: PF00523; fusion\_gly; 1.  
 KW Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal.  
 FT SIGNAL 1 22  
 FT CHAIN 23 537 FUSION GLYCOPROTEIN F0.  
 FT CHAIN 23 101 F2 PROTEIN.  
 FT CHAIN 102 537 F1 PROTEIN.  
 FT TRANSMEM 491 514 POTENTIAL.  
 FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 488 488 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 537 AA; 59366 MW; BA6116E2FBE702 CRC64;

Query Match 23.3%; Score 7; DB 1; Length 537;  
 Best Local Similarity 100.0%; Pred. No. 3.3;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 GEPLVLK 15  
 |||||||  
 Db 434 GEPLVLK 440

RESULT 7  
 YG4L\_YEAST  
 ID YG4L\_YEAST STANDARD; PRT; 110 AA.  
 AC P53305;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)

KW	Ribosomal protein; Complete proteome.
SQ	SEQUENCE 159 AA; 17967 MW; 03FE54B5529DC376 CRC64;
Query Match	
Best Local Similarity 100.0%; Score 6; DB 1; Length 159;	
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY	10 EPLVIK 15 
Db	18 EPLVIK 23
RESULT 9	
YCFA_GUITH	STANDARD; PRT; 181 AA.
ID YCFA_GUITH	PRT; 181 AA.
AC 078467;	
DT 15-DEC-1998 (Rel. 37, Created)	
DT 15-DEC-1998 (Rel. 37, Last sequence update)	
DT 16-OCT-2001 (Rel. 40, Last annotation update)	
DE Photosystem I assembly protein ycf4.	
GN YCF4.	
OS Guillardia theta (Cryptomonas phl).	
OC Chloroplast.	
OX Eukaryota; Cryptophyta; Cryptomonadaceae; Guillardia.	
XX NCBI_TaxID=55529;	
RN [1]	
RP MEDLINE=99128221; PubMed=9929392;	
RA Douglas S.E., Penny S.L.:	
RT "The plastid genome of the cryptophyte alga, Guillardia theta: complete sequence and conserved syteny groups confirm its common ancestry with red algae."	
RL J. Mol. Evol. 48:236-244(1999).	
CC -1 FUNCTION: Seems to be required for the assembly of the photosystem I complex (By similarity).	
CC -1 SUBCELLULAR LOCATION: Thylakoid membrane-associated (By similarity).	
CC -1 SIMILARITY: BELONGS TO THE YCF4 FAMILY.	
CC -----	
CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to <a href="mailto:license@lsb-sib.ch">license@lsb-sib.ch</a> ).	
CC -----	
DR EMBL; AF041468; AAC35658.1; -.	
DR InterPro; IPR003359; Ycf4.	
DR Pfam; PF02392; Ycf4; 1.	
FT Photosynthesis; Thylakoid; Transmembrane; Chloroplast.	
FT TRANSMEM 19 41 POTENTIAL.	
FT TRANSMEM 61 83 POTENTIAL.	
SQ SEQUENCE 181 AA; 20921 MW; 9B74EC86AFEC6F48 CRC64;	
Query Match	
Best Local Similarity 100.0%; Score 6; DB 1; Length 181;	
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY	7 RIGEP L 12 
Db	153 RIGEP L 158
RESULT 10	
YA79_HAEIN	STANDARD; PRT; 210 AA.
ID YA79_HAEIN	PRT; 210 AA.
AC P45023;	
DT 01-OCT-1996 (Rel. 34, Created)	
DT 01-NOV-1997 (Rel. 35, Last sequence update)	
DT 16-OCT-2001 (Rel. 40, Last annotation update)	

DE Hypothetical amino-acid ABC transporter permease protein H10179.  
 GN H10179.  
 OS Haemophilus influenzae.  
 CC Bacteria: Proteobacteria; gamma subdivision; Pasteurellaceae;  
 CC Haemophilus  
 CC NCBI\_TaxID=727;  
 OX  
 RN  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=RD / KW20 / ATCC 51907;  
 RX MEDLINE=95350630; PubMed=7542800;  
 RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,  
 RA Kerelevage A.R., Bult C.J., Tomb J.F., Dougherty B.A., Merrick J.M.,  
 RA McInerney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,  
 RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,  
 RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,  
 RA Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,  
 RA Fier L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,  
 RA Grehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,  
 RA Venter J.C.;  
 RT "Whole-genome random sequencing and assembly of Haemophilus  
 RT influenzae Rd.";  
 RL Science 269:496-512(1995).  
 RN [2]  
 RP REVISIONS.  
 RA White O., Clayton R.A., Kerelevage A.R., Fleischmann R.D.;  
 RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: PROBABLY PART OF A BINDING-PROTEIN-DEPENDENT TRANSPORT  
 CC SYSTEM FOR AN AMINO-ACID. PROBABLY RESPONSIBLE FOR THE  
 CC TRANSLLOCATION OF THE SUBSTRATE ACROSS THE MEMBRANE.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane  
 CC (potential).  
 CC -1- SIMILARITY: WITH INTEGRAL MEMBRANE COMPONENTS OF OTHER BINDING-  
 CC PROTEIN-DEPENDENT TRANSPORT SYSTEMS. BELONGS TO THE HISMO  
 CC SUBFAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: U32788; AAC22735.1; -.  
 DR TIGR: H11079; -.  
 DR InterPro: IPR000515; BPD.transp.  
 DR Pfam: PF00528; BPD.transp. 1.  
 DR PROSITE: PS00402; BPD.TRANSP.INN.MEMBR. 1.  
 KW Hypothetical protein; Transport: Amino-acid transport; Transmembrane;  
 KW Inner membrane; Complete proteome.  
 FT TRANSMEM 10 30 POTENTIAL.  
 FT TRANSMEM 57 77 POTENTIAL.  
 FT TRANSMEM 79 99 POTENTIAL.  
 FT TRANSMEM 177 197 POTENTIAL.  
 SQ SEQUENCE 210 AA; 23393 MW; 662C7C590DC4FDCD CRC64;

Query Match 20.0%; Score 6; DB 1; Length 210;  
 Best Local Similarity 100.0%; Pred. No. 17;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONITA 6  
 Db 167 AONITA 172

RESULT 11  
 VGP8\_EBV STANDARD: PRT; 234 AA.  
 ID VGP8\_EBV  
 AC P03224;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 01-DEC-1992 (Rel. 24, Last annotation update)

DE Probable membrane antigen GP85.  
 GN BDLF3.  
 OS Epstein-Barr virus (strain B95-8) (Human herpesvirus 4).  
 CC Viruses: dsDNA viruses, no RNA stage; Herpesviridae;  
 CC Gammaherpesvirinae; Lymphocryptovirus.  
 CC NCBI\_TaxID=10377;  
 OX  
 RN  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=84270667; PubMed=6087149;  
 RA Baer R., Bankier A.T., Biggin M.D., Deininger P.L., Farrell P.J.,  
 RA Gibson T.J., Hatfull G., Hudson G.S., Satchwell S.C., Segun C.,  
 RA Tufnell P.S., Barrell B.G.;  
 RT "DNA sequence and expression of the B95-8 Epstein-Barr virus genome.";  
 RL Nature 310:207-211(1984).  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: V01555; CAA24835.1; -.  
 DR PIR: A03787; Q05E43.  
 DR PIR: S33040; S33040.  
 KW Membrane; Glycoprotein; Late protein.  
 SQ SEQUENCE 234 AA; 23791 MW; 48D6CED0931119E CRC64;

Query Match 20.0%; Score 6; DB 1; Length 234;  
 Best Local Similarity 100.0%; Pred. No. 19;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONITA 6  
 Db 108 AONITA 113

RESULT 12  
 E434\_ADECT STANDARD: PRT; 259 AA.  
 ID E434\_ADECT  
 AC P87568;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Early E4 30 kDa protein.  
 OS Canine adenovirus type 2 (strain Toronto A 26-61).  
 CC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.  
 CC NCBI\_TaxID=69152;  
 OX  
 RN  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Campbell J.B., Zhao Y.;  
 RT "Complete DNA sequence and genomic organization of canine  
 RT adenovirus type 2.";  
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO THE ADENOVIRUS E4 30 TO 34 KDA PROTEIN  
 CC FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: U77082; AAB38735.1; -.  
 DR Early protein.  
 KW SEQUENCE 259 AA; 30014 MW; 9C966CA011C2A745 CRC64;

Query Match 20.0%; Score 6; DB 1; Length 259;



Best Local Similarity 100.0%; Pred. No. 20;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LVTKCK 17  
|11111|  
Db 178 LVTKCK 183

## RESULT 13

E434\_ADECC

ID E434\_ADECC STANDARD; PRT; 265 AA.

AC 065962;

DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DE Early E4 31 kDa protein.

OS Canine adenovirus type 1 (strain CLU).

OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.

NCBI\_TaxID=69150;

RN [1]

RP SEQUENCE FROM N.A.

RA Campbell J.B., Zhao Y.;

RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE OF 248-265 FROM N.A.

RX MEDLINE=91272490; PubMed=1828920;

RA Dragulev B.F., Sira S., Abouhaider M.G., Campbell J.B.;

RT "Sequence analysis of putative E3 and fiber genomic regions of two

RL strains of canine adenovirus type 1.";

RT Virology 183:298-305(1991).

-1- SIMILARITY: BELONGS TO THE ADENOVIRUS E4 30 TO 34 KDA PROTEIN

CC FAMILY.

-----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC

DR EMBL; U55001; AAB05452.1; -

KM Early protein.

SQ SEQUENCE 265 AA; 30822 MW; 92606E5E30134103 CRC64;

## Query Match

Best Local Similarity 100.0%; Pred. No. 21;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LVTKCK 17  
|11111|  
Db 184 LVTKCK 189

## RESULT 14

E434\_ADECC

ID E434\_ADECC STANDARD; PRT; 265 AA.

AC 026690;

DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)

DE Early E4 31 kDa protein.

OS Canine adenovirus type 1 (strain RI261).

OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.

NCBI\_TaxID=69151;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=92275900; PubMed=9129661;

RA Morrison M.D., Onions D.E., Nicolson L.;

RT "Complete DNA sequence of canine adenovirus type 1.";

RL J. Gen. Virol. 78:873-878(1997).

-1- SIMILARITY: BELONGS TO THE ADENOVIRUS E4 31 TO 34 KDA PROTEIN

-----  
CC FAMILY.

-----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC

DR EMBL; Y07760; CAA69046.1; -

KM Early protein.

SQ SEQUENCE 265 AA; 30737 MW; 14B3DC9DCBD2E15 CRC64;

Query Match  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LVTKCK 17  
|11111|  
Db 184 LVTKCK 189

## RESULT 15

MIND\_GUTH

ID MIND\_GUTH STANDARD; PRT; 269 AA.

AC 078436;

DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Putative septum site-determining protein mind.

GN MIND.

OS Gulliardia theta (Cryptomonas phi).

OG Chloroplast.

OC Eukaryota; Cryptophyta; Cryptomonadaceae; Gulliardia.

NCBI\_TaxID=55529;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=99128221; PubMed=9929392;

RA Douglas S.E., Penny S.L.;

RT "The plastid genome of the cryptophyte alga, Gulliardia theta:

RT complete sequence and conserved syteny groups confirm its common

RT ancestry with red algae.";

RL J. Mol. Evol. 48:236-244(1999).

-1- FUNCTION: ATPASE REQUIRED FOR THE CORRECT PLACEMENT OF THE

DIVISION SITE (BY SIMILARITY).

-1- SIMILARITY: BELONGS TO THE PARA FAMILY. MIND SUBFAMILY.

-----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC

DR EMBL; AF041468; AAC35621.1; -

DR Interpro; IPR000707; PARA.

DR Pfam; PF00991; Para; 1.

KM Cell division; Septation; ATP-binding; Chloroplast.

FT NP\_BIND 10 17 ATP (POTENTIAL)

SQ SEQUENCE 269 AA; 29455 MW; BC363E954E869EA2 CRC64;

Query Match  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GEPLVL 14  
|11111|  
Db 215 GEPLVL 220

Search completed: July 31, 2002, 15:08:15  
Job time: 220 sec

---

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 31, 2002, 15:04:10 ; Search time 25.08 Seconds

(without alignments)  
206.932 Million cell updates/sec

Title: US-08-948-131-1

Perfect score: 30  
Sequence: 1 AQNTFARIGEPVLKCKGAPKKPQRLKWK 30

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 562222 seqs, 172994929 residues

Word size : 0

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

SPTREMBL\_19:\*  
1: sp.archaea:\*  
2: sp.bacteria:\*  
3: sp.fungi:\*  
4: sp.human:\*  
5: sp.invertebrate:\*  
6: sp.mammal:\*  
7: sp.mhc:\*  
8: sp.organelle:\*  
9: sp.phage:\*  
10: sp.plant:\*  
11: sp.podent:\*  
12: sp.virus:\*  
13: sp.vertebrate:\*  
14: sp.unclassified:\*  
15: sp.virus:\*  
16: sp.bacteriap:\*  
17: sp.archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	13	43.3	402	11	035444 mus musculu
2	9	30.0	32	6	09TR01
3	7	23.3	237	5	09V5N7
4	7	23.3	330	16	09K1F6
5	7	23.3	330	16	09JX44
6	7	23.3	595	10	09LOP6
7	7	23.3	742	5	09W322
8	6	20.0	61	5	09NFC5
9	6	20.0	71	5	09N6K0
10	6	20.0	76	5	09N6I0
11	6	20.0	96	10	080389
12	6	20.0	99	10	09FR57
13	6	20.0	101	12	09JH47
14	6	20.0	127	15	09EAJ5
15	6	20.0	155	10	09SC03
16	6	20.0	159	16	0921V4

17	6	20.0	204	16	092H00	092F00 rhizobium m
18	6	20.0	209	16	006630	006630 mycobacteri
19	6	20.0	224	16	092J55	092J55 rhizobium m
20	6	20.0	230	16	09RRE2	09RRE2 delinococcus
21	6	20.0	231	16	092K19	092K19 rhizobium m
22	6	20.0	232	14	091UW4	091UW4 plasmid p1p
23	6	20.0	257	16	006157	006157 mycobacteri
24	6	20.0	259	16	09CCU3	09CCU3 mycobacteri
25	6	20.0	261	2	007711	007711 mycobacteri
26	6	20.0	271	16	067348	067348 aquifex aeo
27	6	20.0	298	10	092S04	092S04 arabidopsis
28	6	20.0	298	16	09A7U8	09A7U8 cauliobacter
29	6	20.0	318	16	098707	098707 rhizobium l
30	6	20.0	326	16	09HX11	09HX11 pseudomonas
31	6	20.0	334	5	09V6W0	09V6W0 drosophila
32	6	20.0	334	16	09HXF7	09HXF7 pseudomonas
33	6	20.0	339	11	09QYV4	09QYV4 rattus norv
34	6	20.0	339	11	062708	062708 rattus norv
35	6	20.0	359	2	088036	088036 streptomyce
36	6	20.0	359	8	09TUR6	09TUR6 prototheca
37	6	20.0	377	16	097TK0	097TK0 clostridium
38	6	20.0	387	10	09XIS0	09XIS0 arabidopsis
39	6	20.0	389	9	038644	038644 bacterioph
40	6	20.0	392	2	09FC10	09FC10 streptomyce
41	6	20.0	411	10	09M3H9	09M3H9 cicier ariet
42	6	20.0	426	5	0917W7	0917W7 drosophila
43	6	20.0	433	2	052912	052912 rhizobium m
44	6	20.0	433	16	0927A1	0927A1 rhizobium m
45	6	20.0	452	10	09LHM5	09LHM5 arabidopsis

## ALIGNMENTS

RESULT	1	PRELIMINARY:	PRT:	402 AA.
ID	035444			
AC	035444			
DT	01-JAN-1998 (TREMBLrel. 05, Created)			
DT	01-JAN-1998 (TREMBLrel. 05, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	RAGE.			
GN	RAGE.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Rosen L., Mahatras G., Qin S., Ahearn M.E., Dankers C., Lasky S.,			
RA	Loreta C., Schmidt S., Tipton S., Tralcoff R., Zackrone K., Hood L.,			
RT	"Sequence of the mouse major histocompatibility locus class III			
RT	region."			
RL	Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.			
DR	EMBL: AF030001; AAB82007.1; "			
DR	InterPro: IPR003598; Ig_c2.			
DR	InterPro: IPR003600; Ig_like.			
DR	InterPro: IPR003006; Ig_MHC.			
DR	Pfam: PF00047; Ig_3.			
DR	SMART: SM00408; IGC2; 1.			
DR	SMART: SM00410; IG_Like; 1.			
DR	PROSITE: PS00290; IG_MHC; UNKNOWN_1.			
KW	Immunoglobulin domain.			
SC	SEQUENCE 402 AA; 42653 MW; DBFDC50A6C8CB902 CRC64;			

Query Match 43.3%; Score 13; DB 11; Length 402;

Best Local Similarity 100.0%; Pred. No. 2.5e-06; Mismatches 0; Indels 0; Gaps 0;

QY 2 QNTFARIGEPVL 14  
IIIIIIIIIIIIII  
Db 24 QNTFARIGEPVL 36

```

RESULT 2
Q9TRQ1 PRELIMINARY; PRT; 32 AA.
ID 09TRQ1
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE 35 KDA ADVANCED GLYCOSYLATION END PRODUCT BINDING PROTEIN (FRAGMENT).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=92340546; PubMed=1321822;
RA Schmidt A.M., Viana M., Gerlach M., Brett J., Ryan J., Kao J.,
RA Esposto C., Hegarty H., Hurley W., Claus M.,
RT Isolation and characterization of two binding proteins for advanced
RT glycosylation end products from bovine lung which are present on the
RT endothelial cell surface.*;
RL J. Biol. Chem. 267:14987-14997(1992).
SQ SEQUENCE 32 AA; 3507 MW; AEC3147CE5B3D91 CRC64;

```

```

Query Match 30.0%; Score 9; DB 6; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.0074;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 17 KGAPKPPQ 25
Db 17 KGAPKPPQ 25

```

```

RESULT 3
Q9VSN7 PRELIMINARY; PRT; 237 AA.
ID 09VSN7
AC Q9VSN7;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE CG12934 PROTEIN.
GN CG12934.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle J.R.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brendon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abrell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandal D., Bolshakov S.,
RA Botkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA Butts K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Doonan K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunlov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz S., Ferriere S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garcia N.S., Gelbart W.M., Glasser K.,
RA Glodde N.L., Gong F., Gorrell J.H., Gu Z., Guan X., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

```

```

RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laake P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusken D.R., Pacled J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spler E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svyrskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL: AE003828; AAF58764.1;
DR Flybase: FBgn0033541; CG12934.
SQ SEQUENCE 237 AA; 27208 MW; C05010AD183FAE7 CRC64;

```

```

Query Match 23.3%; Score 7; DB 5; Length 237;
Best Local Similarity 100.0%; Pred. No. 6.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 22 KPPORLE 28
Db 106 KPPORLE 112

```

```

RESULT 4
Q9K1F6 PRELIMINARY; PRT; 330 AA.
ID 09K1F6
AC 09K1F6;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE RIBOSOMAL LARGE SUBUNIT PSEUDOURIDINE SYNTHASE C.
GN NMB0198.
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58 / SEROGROUP B;
RX MEDLINE=20175755; PubMed=10710307;
RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
RA Nelson W.C., Gwin M.L., DeBoy O., Peterson J.D., Hickey E.K.,
RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
RA Mason T., Ciecko A., Parksey D.S., Blair E., Cifton H., Clark E.B.,
RA Cotton M.D., Uitterlind T.R., Khouri H., Qin H., Yamashiro J.,
RA Gill J., Scarlato V., Maignani V., Pizzo M., Grandi G., Sun L.,
RA Smith H.O., Fraser C.M., Moxon E.R., Rappelli R., Venter J.C.;
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
RT MC58."
RL Science 287:1809-1815(2000).
DR EMBL: AE002377; AAF40655.1;
DR TIGR: NMB0198;
DR InterPro: IPR000613; Pseudou_synth.
DR InterPro: IPR002990; PSI_RLU.
DR InterPro: IPR002942; S4.
DR Pfam: PF00849; Pseudou_synth.2; 1.
DR ProDom: PD001819; Pseudou_synth; 1.
DR SMART: SM00363; S4; 1.
DR PROSITE: PS01129; PSI_RLU; 1.
KW Complete proteome.
SQ SEQUENCE 330 AA; 36682 MW; F2058C52ACFA43BC CRC64;

```

Query Match  
Best Local Similarity 23.3%; Score 7; DB 16; Length 330;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 GEPLVLR 15  
|||||||

DB 304 GEPLVLR 310

RESULT 5  
ID O9JX44 PRELIMINARY; PRT; 330 AA.  
AC O9JX44;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE RIBOSOMAL LARGE SUBUNIT PSEUDOURIDINE SYNTHASE C (EC 4.2.1.70).  
GN RLOC OR NMA0070.  
OS Neisseria meningitidis (serogroup A).  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=56599;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=22491 / SEROGROUP A / SEROTYPE 4A;  
RX MEDLINE=20222556; PubMed=10761919;  
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,  
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,  
RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holtroyd S.,  
RA Jagers K., Leather S., Moule S., Mungall K., Quail M.A.,  
RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,  
RA Whitehead S., Spratt B.G., Barrall B.G.;  
RT "Complete DNA sequence of a serogroup A strain of Neisseria  
meningitidis 22491".  
RL Nature 404:502-506(2000).  
DR EMBL; AL162752; CAB83386.1; -  
DR InterPro; IPR000613; Pseudou\_synth.  
DR InterPro; IPR002990; PSI\_RLU.  
DR InterPro; IPR002942; S4.  
DR Pfam; PF00849; Pseudou\_synth\_2; 1.  
DR PRODOM; PD001819; Pseudou\_synth; 1.  
DR SMART; SM00363; S4; 1.  
DR PROSITE; PS01129; PSI\_RLU; 1.  
KW Lysase; Complete proteome.  
SQ SEQUENCE 330 AA; 36768 MW; 9B1AB94890F675EA CRC64;

Query Match  
Best Local Similarity 23.3%; Score 7; DB 16; Length 330;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 GEPLVLR 15  
|||||||

DB 304 GEPLVLR 310

RESULT 6  
ID O9LOP6 PRELIMINARY; PRT; 595 AA.  
AC O9LOP6;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE F24B9.20.  
GN F24B9.20.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosidis II; Brassicales; Brassicaceae; Arabidopsis.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CV. COLUMBIA;  
RA Liu S., Yu G., Sakano H., Jhaveri A., Lee J., Lenz C., Pham P.,

RA Toriumi M., Chin C., Choi E., Chlou J., Gonzalez A., Chung M.,  
RA Hong B., Koo T., Li J., Liu A., Vaysberg M., Alcafi H., Brooks S.,  
RA Buehler E., Chao Q., Conn L., Conway A.B., Hansen N.,  
RA Johnson-Hopson C., Khan S., Kim C., Lam B., Nguyen M., Palm C.,  
RA Shun P., Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.;  
RT "The sequence of BAC F24B9 from Arabidopsis thaliana chromosome 1.";  
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.

RN [12]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CV. COLUMBIA;  
RA Theologis A.;  
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AC007583; AAF75084.1; -  
SQ SEQUENCE 595 AA; 63982 MW; FF5B15FB2B8B7E CRC64;

Query Match  
Best Local Similarity 23.3%; Score 7; DB 10; Length 595;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 RIGEPV 13  
|||||||

DB 550 RIGEPV 556

RESULT 7  
ID O9W322 PRELIMINARY; PRT; 742 AA.  
AC O9W322;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE CG3106 PROTEIN (GH10201P).  
GN CG3106.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BERKELEY;  
RX MEDLINE=20196006; PubMed=10731132;  
RA Adams M.D., Celiker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,  
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,  
RA Burlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferriz C., Ferriere S., Fleischmann W.,  
RA Foster C., Gabriellian A.E., Gary N.S., Gelbart W.M., Glasser K.,  
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegam C.,  
RA Jalaal M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., Meperson D.,  
RA Mekulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclad J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheefer F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of *Drosophila melanogaster*.";  
 RL Science 287:2185-2195(2000).  
 RN [12]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Y, CN BW SP;  
 RA Stapleton M., Brokstein P., Hong L., Abpayani A., Carlson J.,  
 RA Champe M., Chavez C., Dorsett V., Farfan D., Flise E., George R.,  
 RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,  
 RA Nuno J., Paclé J., Paragas V., Park S., Phouanavong S., Wan K.,  
 RA Yu C., Lewis S.E., Rubin G.M., Celinker S.;  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AE003448; AAF6515.1; -  
 DR EMBL: AY058329; AAL13558.1; -  
 DR FlyBase; FBgn030148; CG3106.  
 DR InterPro; IPR003862; UPP0063.  
 DR Pfam; PF02712; UPP0063; 1.  
 SQ SEQUENCE 742 AA; 84476 MW; EFF31DF7DC6DE02D CRC64;

Query Match 23.3%; Score 7; DB 5; Length 742;  
 Best Local Similarity 100.0%; Pred. No. 17;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 17 KGAPKK 23  
 |||||  
 DB 254 KGAPKKP 260

RESULT 8  
 Q9NFJ5 PRELIMINARY; PRT; 61 AA.  
 AC Q9NFJ5;  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)  
 DE HISTONE H1.  
 GN H1A61.  
 OS Trypanosoma brucei brucei.  
 OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.  
 OX NCBI\_TaxID=5702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=TREU 927/4;  
 RA Grueter E.;  
 RL Thesis (2000), Department of Parasitology, Institute of Zoology,  
 RL SWITZERLAND.  
 DR EMBL: AJ287603; CAB76188.1; -  
 DR EMBL: AJ287603; CAB76188.1; -  
 SQ SEQUENCE 61 AA; 6012 MW; 7B66DA10A7D3B93 CRC64;

Query Match 20.0%; Score 6; DB 5; Length 61;  
 Best Local Similarity 100.0%; Pred. No. 26;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 17 KGAPKK 22  
 |||||  
 DB 30 KGAPKK 35

RESULT 9  
 Q9N6KO PRELIMINARY; PRT; 71 AA.  
 AC Q9N6KO;  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)  
 DE HISTONE H1.

GN H1E71 OR H1A71.  
 OS Trypanosoma brucei brucei.  
 OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.  
 OX NCBI\_TaxID=5702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=TREU 927/4;  
 RA Grueter E.;  
 RL Thesis (2000), Department of Parasitology, Institute of Zoology,  
 DR EMBL: AJ400881; CAB90839.1; -  
 DR EMBL: AJ287600; CAB76185.1; -  
 SQ SEQUENCE 71 AA; 7005 MW; 478C7B6994847C80 CRC64;

Query Match 20.0%; Score 6; DB 5; Length 71;  
 Best Local Similarity 100.0%; Pred. No. 29;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 17 KGAPKK 22  
 |||||  
 DB 30 KGAPKK 35

RESULT 10  
 Q9N6IO PRELIMINARY; PRT; 76 AA.  
 AC Q9N6IO;  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
 DE HISTONE H1.  
 GN H1E76 OR H1F76.  
 OS Trypanosoma brucei brucei.  
 OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.  
 OX NCBI\_TaxID=5702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=TREU 927/4;  
 RA Grueter E.;  
 RL Thesis (2000), Department of Parasitology, Institute of Zoology,  
 RL SWITZERLAND.  
 DR EMBL: AJ287605; CAB76190.1; -  
 DR EMBL: AJ287601; CAB76186.1; -  
 DR InterPro; IPR001386; Linker\_histone.  
 DR PRINTS; PR00624; HISTONEH5.  
 SQ SEQUENCE 76 AA; 7573 MW; 6079EFA982B50767 CRC64;

Query Match 20.0%; Score 6; DB 5; Length 76;  
 Best Local Similarity 100.0%; Pred. No. 31;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 17 KGAPKK 22  
 |||||  
 DB 30 KGAPKK 35

RESULT 11  
 O80389 PRELIMINARY; PRT; 96 AA.  
 AC O80389;  
 DT 01-NOV-1998 (TREMBlrel. 08, Created)  
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
 DE CYSTEIN PROTEINASE INHIBITOR.  
 OS Cucumis sativus (Cucumber).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.  
 OX NCBI\_TaxID=3659;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Yamakawa S.;

"Cysteine proteinase inhibitor."  
 RT Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AB014760; BAA28867.1; -  
 DR InterPro: IPR000101; Cystatin.  
 DR InterPro: IPR003243; Cystatin\_C\_M.  
 DR Pfam: PF00031; Cystatin\_1.  
 DR ProDom: PD001231; Cystatin\_C\_M; 1.  
 DR SMART: SM00043; CY: 1.  
 DR PROSITE: PS00287; CYSTATIN; UNKNOWN\_1.  
 DR SEQUENCE 96 AA; 10973 MW; 027252E14BB6C4F4 CRC64;  
 SQ  
 Query Match 20.0%; Score 6; DB 10; Length 96;  
 Best Local Similarity 100.0%; Pred. No. 38;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 12 LVLRCK 17  
 DB 59 LVLRCK 64  
 RESULT 12  
 Q9FR57 PRELIMINARY; PRT; 99 AA.  
 ID Q9FR57;  
 AC Q9FR57;  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DE SELF-PRUNING INTERACTING PROTEIN 1.  
 OS Lycopersicon esculentum (Tomato).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.  
 OC NCBI\_TaxID=4081;  
 RN [1]  
 RM SEQUENCE FROM N.A.  
 RC STRAIN-CV. VENT;  
 RA Punell L., Guttinger T., Hareven D., Ben-Naim O., Ron N., Adir N.,  
 RA Lifschitz E.,  
 RT "Tomato SP-interacting proteins define a conserved signalling system  
 RT that regulates shoot architecture and flowering.";  
 RL Plant Cell 0:0-0(2001).  
 DR EMBL: AF175963; AAC43410.1; -  
 SO SEQUENCE 99 AA; 11408 MW; E55F6975B7BA97A3 CRC64;  
 SQ  
 Query Match 20.0%; Score 6; DB 10; Length 99;  
 Best Local Similarity 100.0%; Pred. No. 39;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 18 GAPKKP 23  
 DB 45 GAPKKP 50  
 RESULT 13  
 Q9JH47 PRELIMINARY; PRT; 101 AA.  
 ID Q9JH47;  
 AC Q9JH47;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DE SPART CODON IS NOT IDENTIFIED (FRAGMENT).  
 GN EA.  
 OS Human papillomavirus type 69.  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 OC Papillomavirus.  
 OX NCBI\_TaxID=37121;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Matsukura T., Sata T.;  
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
 DT [2]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=20087389; PubMed=10618284;  
 RA Kino N., Sata T., Sato Y., Sugase M., Matsukura T.;  
 RT "Molecular cloning and nucleotide sequence analysis of a novel human  
 RT papillomavirus (type 82) associated with vaginal intraepithelial  
 RT neoplasia."  
 RL Clin. Diagn. Lab. Immunol. 7:91-95(2000).  
 DR EMBL: AB027020; BAA90731.1; -  
 DR InterPro: IPR003861; Papilloma\_E4.  
 DR Pfam: PF02711; Pap\_E4; 1.  
 DR NON\_TER 1  
 FT 1  
 SQ SEQUENCE 101 AA; 11267 MW; 32899BE169CAC792 CRC64;  
 SQ  
 Query Match 20.0%; Score 6; DB 12; Length 101;  
 Best Local Similarity 100.0%; Pred. No. 40;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 18 GAPKKP 23  
 DB 39 GAPKKP 44  
 RESULT 14  
 Q9EAJ5 PRELIMINARY; PRT; 127 AA.  
 ID Q9EAJ5;  
 AC Q9EAJ5;  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE PROTEASE (FRAGMENT).  
 GN POL.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OC NCBI\_TaxID=11676;  
 RN [1]  
 RM SEQUENCE FROM N.A.  
 RC STRAIN-99-117635;  
 RX MEDLINE=21178648; PubMed=11282016;  
 RA Barlow K.L., Talt I.D., Cane P.A., Pillay D., Clewley J.P.;  
 RT "Recombinant strains of HIV type 1 in the United Kingdom."  
 RT AIDS Res. Hum. Retroviruses 17:467-474(2001).  
 CC -1- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY A2; ALSO  
 CC KNOWN AS THE RETROPEPSIN FAMILY.  
 DR EMBL: AJ296662; CAC03693.1; -  
 DR HSP; P04584; IPHV.  
 DR InterPro: IPR001969; Asp\_protease.  
 DR InterPro: IPR001995; Asp\_prot\_retrov.  
 DR Pfam: PF00077; rvp; 1.  
 DR PROSITE: PS00141; ASP\_PROTEASE; 1.  
 DR PROSITE: PS50175; ASP\_PROT\_RETROV; 1.  
 KW Aspartyl protease; Hydrolase.  
 FT NON\_TER 1  
 FT 127  
 SQ SEQUENCE 127 AA; 13648 MW; CEAF2745863D5F4 CRC64;  
 SQ  
 Query Match 20.0%; Score 6; DB 15; Length 127;  
 Best Local Similarity 100.0%; Pred. No. 48;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 ITARIG 9  
 DB 39 ITARIG 44  
 RESULT 15  
 Q9SC03 PRELIMINARY; PRT; 155 AA.  
 ID Q9SC03;  
 AC Q9SC03;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

DE HYPOTHETICAL 17.0 KDA PROTEIN.  
GN T4D2.10.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurossids II; Brassicales; Brassicaceae; Arabidopsis.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Nyakatura G., Partmann B., Dauner D., Sterr W., Holland R.,  
RA Weichselgartner M., Mewes H.W., Lemcke K., Mayer K.F.X., Quettier F.,  
RA Salanoubat M.;  
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA EU Arabidopsis sequencing project;  
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AL132958; CAB64211.1; -  
DR InterPro: IPR000922; Gal\_lectin.  
DR Pfam: PF02140; Gal\_lectin; 1.  
DR ProDom: PD005612; Gal\_lectin; 1.  
DR ProSITE: PS50228; SUEL\_LLECTIN; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 155 AA; 16990 MW; 815302F74AE2EFCB CRC64;

Query Match 20.0%; Score 6; DB 10; Length 155;  
Best Local Similarity 100.0%; Pred. No. 57;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 KCKGAP 20  
| | | | |  
DB 139 KCKGAP 144

Search completed: July 31, 2002, 15:08:00  
Job time: 230 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 31, 2002, 15:03:45 ; Search time 12.99 Seconds

(without alignments)  
56.410 Million cell updates/sec

Title: US-08-948-131-1

Perfect score: 30  
Sequence: 1 AONTARIGEPLVLCGAKPKPPQRLKWK 30

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 231628 seqs, 24425594 residues

Word size : 0

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Issued Patents-AA:

1: /cgn2\_6/ptodata/2/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/2/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/2/1aa/PCRTOS.COMB.pep:\*  
6: /cgn2\_6/ptodata/2/1aa/Backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	100.0	318	2	US-08-633-148-4
2	30	100.0	340	2	US-08-633-148-2
3	23	76.7	278	2	US-08-432-016-5
4	23	76.7	278	2	US-08-684-594-5
5	16	53.3	16	2	US-08-633-148-18
6	15	50.0	15	2	US-08-633-148-12
7	10	33.3	10	2	US-08-633-148-5
8	10	33.3	10	2	US-08-633-148-13
9	6	20.0	10	4	US-08-685-558A-2
10	6	20.0	479	1	US-08-416-788-2
11	6	20.0	481	1	US-08-173-436A-2
12	6	20.0	481	1	US-08-748-485-8
13	6	20.0	513	4	US-08-685-558A-18
14	6	20.0	741	1	US-08-277-231A-4
15	6	20.0	741	1	US-08-473-750-7
16	6	20.0	741	2	US-08-477-326-7
17	6	20.0	1103	3	US-09-162-372-1
18	6	20.0	1103	4	US-09-467-946-1
19	6	20.0	1958	1	US-07-945-283-2
20	5	16.7	11	1	US-08-336-343A-23
21	5	16.7	14	1	US-08-137-117D-153
22	5	16.7	14	1	US-08-137-117D-155
23	5	16.7	14	1	US-08-137-117D-158
24	5	16.7	14	2	US-08-436-717-153
25	5	16.7	14	2	US-08-436-717-155
26	5	16.7	14	2	US-08-436-717-158
27	5	16.7	20	4	US-08-602-999A-134

28	5	16.7	20	4	US-09-242-131A-1	Sequence 1, Appl
29	5	16.7	20	4	US-09-615-283-1	Sequence 1, Appl
30	5	16.7	22	4	US-09-242-131A-7	Sequence 7, Appl
31	5	16.7	22	4	US-09-615-283-7	Sequence 7, Appl
32	5	16.7	24	4	US-08-525-539A-22	Sequence 22, Appl
33	5	16.7	26	2	US-08-637-759B-126	Sequence 326, App
34	5	16.7	26	3	US-08-871-355A-126	Sequence 326, App
35	5	16.7	26	4	US-08-525-539A-20	Sequence 20, Appl
36	5	16.7	26	4	US-09-201-945-326	Sequence 326, App
37	5	16.7	49	4	US-09-085-305-22	Sequence 22, Appl
38	5	16.7	59	4	US-09-085-305-21	Sequence 21, Appl
39	5	16.7	63	2	US-08-637-759B-191	Sequence 191, App
40	5	16.7	63	3	US-08-871-355A-191	Sequence 191, App
41	5	16.7	63	4	US-09-201-945-191	Sequence 191, App
42	5	16.7	72	4	US-09-188-930-133	Sequence 153, App
43	5	16.7	72	4	US-09-188-930-304	Sequence 304, App
44	5	16.7	75	4	US-09-450-072-70	Sequence 70, Appl
45	5	16.7	80	4	US-09-085-305-23	Sequence 23, Appl

## ALIGNMENTS

Result 1  
US-08-633-148-4  
Sequence 4, Application US/08633148  
Patent No. 5864018  
GENERAL INFORMATION:  
APPLICANT: MORSE, MICHAEL J.  
APPLICANT: MATSUSHITA, MARIKO  
APPLICANT: HOLLANDER, DORIS A.  
TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION  
TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP  
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: U.S.A.  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/633,148  
FILING DATE: 16-APR-1996  
CLASSIFICATION: A35  
ATTORNEY/AGENT INFORMATION:  
NAME: MORPHY ESO., MATTHEW B.  
REGISTRATION/DOCKET NUMBER: 39,787  
REFERENCE/DOCKET NUMBER: 014618-0056000US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 318 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-633-148-4

Query Match 100.0%, Score 30; DB 2; Length 318;  
Best Local Similarity 100.0%, Pred. No. 1.3e-24;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 AONITARIGEPVLKCKGAPKPPQRLWK 30

RESULT 2

US-08-633-148-2

Sequence 2, Application US/08633148

Patent No. 5864018

GENERAL INFORMATION:

APPLICANT: MORSE, MICHAEL J.

APPLICANT: NAGASHIMA, MARIKO

APPLICANT: HOLLANDER, DORIS A.

TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION

TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESSES:

ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP

STREET: TWO EMBARCADERO CENTER, 8TH FLOOR

CITY: SAN FRANCISCO

STATE: CALIFORNIA

COUNTRY: U.S.A.

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/633,148

FILING DATE: 16-APR-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: MURPHY ESO, MATTHEW B.

REGISTRATION NUMBER: 39,787

REFERENCE/DOCKET NUMBER: 014618-005600US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 326-2400

TELEFAX: (415) 326-2422

INFORMATION FOR SEQ. ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 340 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-633-148-2

Query Match

Best Local Similarity 100.0%; Score 30; DB 2; Length 340;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AONITARIGEPVLKCKGAPKPPQRLWK 30

Db 23 AONITARIGEPVLKCKGAPKPPQRLWK 52

RESULT 3

US-08-432-016-5

Sequence 5, Application US/08432016

Patent No. 5968768

GENERAL INFORMATION:

APPLICANT: HAYNES, BARTON F.

APPLICANT: ARUFFO, ALEJANDRO

APPLICANT: PATEL, DHAVALKUMAR

APPLICANT: BOWEN, MICHAEL A.

APPLICANT: MAROUARDT, HANS

TITLE OF INVENTION: CD6 LIGAND

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESSES:

ADDRESSEE: NIXON & VANDERHYTE P. C.

STREET: 1100 NORTH GLEBE ROAD

CITY: ARLINGTON

STATE: VIRGINIA

COUNTRY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/432,016

FILING DATE: 01-MAY-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/333,350

FILING DATE: 02-NOV-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/143,903

FILING DATE: 02-NOV-1993

ATTORNEY/AGENT INFORMATION:

NAME: WILSON, MARY J.

REGISTRATION NUMBER: 32,955

REFERENCE/DOCKET NUMBER: 1579-95

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 816-4000

TELEFAX: (703) 816-4100

INFORMATION FOR SEQ. ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 278 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-432-016-5

Query Match

Best Local Similarity 76.7%; Score 23; DB 2; Length 278;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 IGEPLVLKCKGAPKPPQRLWK 30

Db 1 IGEPLVLKCKGAPKPPQRLWK 23

RESULT 4

US-08-684-594-5

Sequence 5, Application US/08684594

Patent No. 5998172

GENERAL INFORMATION:

APPLICANT: HAYNES, BARTON F.

APPLICANT: ARUFFO, ALEJANDRO

APPLICANT: PATEL, DHAVALKUMAR

APPLICANT: BOWEN, MICHAEL A.

APPLICANT: MAROUARDT, HANS

TITLE OF INVENTION: CD6 LIGAND

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESSES:

ADDRESSEE: NIXON & VANDERHYTE P. C.

STREET: 1100 NORTH GLEBE ROAD

CITY: ARLINGTON

STATE: VIRGINIA

COUNTRY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/684,594

FILING DATE: 18-JUL-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/432,016

FILING DATE: 01-MAY-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/333,350  
FILING DATE: 02-NOV-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/143,903  
FILING DATE: 02-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: WILSON, MARY J.  
REGISTRATION NUMBER: 32,955  
REFERENCE/DOCKET NUMBER: 1579-112  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 816-4000  
TELEFAX: (703) 816-4100  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 278 amino acids  
TYPE: amino acid  
STRANDEDNESS: linear  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-684-594-5

Query Match 76.7%; Score 23; DB 2; Length 278;  
Best Local Similarity 100.0%; Pred. No. 3.1e-17;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 IGEPLVLCGKAGKPPORLEWK 30  
DB 1 IGEPLVLCGKAGKPPORLEWK 23

RESULT 5  
US-08-633-148-18  
Sequence 18, Application US/08633148  
Patent No. 5864018  
GENERAL INFORMATION:  
APPLICANT: MORSE, MICHAEL J.  
APPLICANT: NAGASHIMA, MARIKO  
TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION  
TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP  
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: U.S.A.  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/633,148  
FILING DATE: 16-APR-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MURPHY ESQ., MATTHEW B.  
REGISTRATION NUMBER: 39,787  
REFERENCE/DOCKET NUMBER: 014618-005600US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: peptide  
US-08-633-148-18

Query Match 53.3%; Score 16; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 8.2e-11;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AONITARISEPLVLC 16  
DB 1 AONITARISEPLVLC 16

RESULT 6  
US-08-633-148-12  
Sequence 12, Application US/08633148  
Patent No. 5864018  
GENERAL INFORMATION:  
APPLICANT: MORSE, MICHAEL J.  
APPLICANT: NAGASHIMA, MARIKO  
TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION  
TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP  
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: U.S.A.  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/633,148  
FILING DATE: 16-APR-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MURPHY ESQ., MATTHEW B.  
REGISTRATION NUMBER: 39,787  
REFERENCE/DOCKET NUMBER: 014618-005600US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-633-148-12

Query Match 50.0%; Score 15; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 8.9e-10;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AONITARISEPLVLC 15  
DB 1 AONITARISEPLVLC 15

RESULT 7  
US-08-633-148-5  
Sequence 5, Application US/08633148  
Patent No. 5864018  
GENERAL INFORMATION:  
APPLICANT: MORSE, MICHAEL J.  
APPLICANT: NAGASHIMA, MARIKO

APPLICANT: HOLLANDER, DORIS A.  
TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION  
END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: TOWNSEND & TOWNSENT & CREW LLP  
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: U.S.A.  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/633,148  
FILING DATE: 16-APR-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MURPHY ESQ., MATTHEW B.  
REGISTRATION NUMBER: 39,787  
REFERENCE/DOCKET NUMBER: 014618-005600US  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-633-148-5

Query Match 33.3%; Score 10; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.00013;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 CKGAPKRPQ 25  
|||||  
Db 1 CKGAPKRPQ 10

RESULT 8  
US-08-633-148-13  
Sequence 13, Application US/08633148  
Patent No. 5864018  
GENERAL INFORMATION:  
APPLICANT: MORSE, MICHAEL J.  
APPLICANT: NAGASHIMA, MARIKO  
APPLICANT: HOLLANDER, DORIS A.  
TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION  
END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: TOWNSEND & TOWNSENT & CREW LLP  
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: U.S.A.  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/633,148  
FILING DATE: 16-APR-1996  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: MURPHY ESQ., MATTHEW B.  
REGISTRATION NUMBER: 39,787  
REFERENCE/DOCKET NUMBER: 014618-005600US  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-633-148-13

Query Match 33.3%; Score 10; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.00013;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 CKGAPKRPQ 25  
|||||  
Db 1 CKGAPKRPQ 10

RESULT 9  
US-08-685-558A-2  
Sequence 2, Application US/0868558A  
Patent No. 6235081  
GENERAL INFORMATION:  
APPLICANT: SHIMOMURA, Takeshi  
APPLICANT: KAWAGUCHI, Toshiya  
APPLICANT: KITAMURA, Naomi  
APPLICANT: MIYAZAWA, Keiji  
TITLE OF INVENTION: NOVEL PROTEIN, DNA CODING FOR SAME  
AND METHOD OF PRODUCING THE PROTEIN  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SUGHRUE, MION, ZINN, MACPHEAR & SEAS  
STREET: 2100 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/685,558A  
FILING DATE: 24-JUL-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JPA Hei 7-187135  
FILING DATE: 24-JUL-1995  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: Internal fragment  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
STRAIN: MKN45  
US-08-685-558A-2

Query Match 20.0%; Score 6; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 EPLVLR 15  
111111  
DB 5 EPLVLR 10

RESULT 10  
US-08-416-788-2  
; Sequence 2, Application US/08416788  
; Patent No. 5780245  
; GENERAL INFORMATION:  
; APPLICANT: Maroteaux, Luc  
; TITLE OF INVENTION: No. 5780245e1 Polypeptides Having a Serotonin  
; TITLE OF INVENTION: Receptor Activity, Nucleic Acids Coding for These  
; TITLE OF INVENTION: Polypeptides and Uses  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Rhone-Poulenc Rorer Inc.  
; STREET: 500 Arcola Road, 3C43  
; CITY: Collegeville  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19426-0107  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/416,788  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: NO PCT/FR93/01012  
; FILING DATE: 13-OCT-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 92-12280  
; FILING DATE: 14-OCT-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, Julie K.  
; REGISTRATION NUMBER: 38,619  
; REFERENCE/DOCKET NUMBER: EX92008-US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (610)454-3839  
; TELEFAX: (610)454-3808  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 479 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-416-788-2

Query Match 20.0%; Score 6; DB 1; Length 479;  
Best Local Similarity 100.0%; Pred. No. 55;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 22 KPPORL 27  
111111  
DB 253 KPPORL 258

RESULT 11  
US-08-173-436A-2  
; Sequence 2, Application US/08173436A  
; Patent No. 5698444  
; GENERAL INFORMATION:  
; APPLICANT: Baetz, Melvyn  
; APPLICANT: Kursat, Jonathan D.  
; TITLE OF INVENTION: SEROTONIN RECEPTOR PROTEIN AND RELATED  
; TITLE OF INVENTION: NUCLEIC ACID COMPOUNDS  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Eli Lilly and Company  
STREET: Lilly Corporate Center/Patent Division  
CITY: Indianapolis  
STATE: IN  
COUNTRY: US  
ZIP: 46285  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/173,436A  
; FILING DATE: 23-DEC-1993  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Gaylo, Paul J.  
; REGISTRATION NUMBER: 36,808  
; REFERENCE/DOCKET NUMBER: X-9367  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 317-276-0756  
; TELEFAX: 317-276-3861  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 481 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-173-436A-2

Query Match 20.0%; Score 6; DB 1; Length 481;  
Best Local Similarity 100.0%; Pred. No. 56;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 22 KPPORL 27  
111111  
DB 254 KPPORL 259

RESULT 12  
US-08-748-485-8  
; Sequence 8, Application US/08748485  
; Patent No. 5817480  
; GENERAL INFORMATION:  
; APPLICANT: Au-Young, Janice  
; APPLICANT: Guegler, Karl J.  
; APPLICANT: Goll, Surya K.  
; APPLICANT: Murty, Lynn E.  
; TITLE OF INVENTION: NOVEL HISTAMINE H2 RECEPTOR  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: US  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/748,485  
; FILING DATE: Herewith  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0159 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0553  
TELEFAX: 415-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 481 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: 475198  
US-08-748-485-8

Query Match 20.0%; Score 6; DB 2; Length 481;  
Best Local Similarity 100.0%; Pred. No. 56;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 22 KPPQRL 27  
Db 254 KPPQRL 259

RESULT 13  
US-08-685-558A-18  
Sequence 18, Application US/08685558A  
Patent No. 6225081  
GENERAL INFORMATION:  
APPLICANT: SHIMOMURA, Takeshi  
APPLICANT: KAWAGUCHI, Toshiya  
APPLICANT: KITAMURA, Naomi  
APPLICANT: MIYAZAWA, Keiji  
TITLE OF INVENTION: NOVEL PROTEIN, DNA CODING FOR SAME  
TITLE OF INVENTION: AND METHOD OF PRODUCING THE PROTEIN  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SUGHRUE, MIOM, ZINN, MACPHEAK & SEAS  
STREET: 2100 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/685,558A  
FILING DATE: 24-JUL-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JPA Hei 7-187135  
FILING DATE: 24-JUL-1995  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 513 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
STRAIN: MKN45  
US-08-685-558A-18

Query Match 20.0%; Score 6; DB 4; Length 513;  
Best Local Similarity 100.0%; Pred. No. 59;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 EPLVLR 15  
Db 177 EPLVLR 182

RESULT 14  
US-08-277-231A-4  
Sequence 4, Application US/08277231A  
Patent No. 5643725  
GENERAL INFORMATION:  
APPLICANT: Green, Bruce A.  
APPLICANT: Brinton, Charles C.  
TITLE OF INVENTION: Sequence and Analysis of LKP P11n  
Patent No. 5643725  
TITLE OF INVENTION: Structural Genes and The LKP P11 Operon of No. 5643725cypa  
TITLE OF INVENTION: Haemophilus Influenzae  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Millitia Drive  
CITY: Lexington  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/277,231A  
FILING DATE: 19-JUL-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Carroll, Alice O.  
REGISTRATION NUMBER: 32,542  
REFERENCE/DOCKET NUMBER: ACC94-02  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 861-6240  
TELEFAX: (617) 861-9540  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 741 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-277-231A-4

Query Match 20.0%; Score 6; DB 1; Length 741;  
Best Local Similarity 100.0%; Pred. No. 79;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 TARGE 10  
Db 157 TARGE 162

RESULT 15  
US-08-473-750-7  
Sequence 7, Application US/08473750  
Patent No. 5834187  
Patent No. 5834187 5786143  
GENERAL INFORMATION:  
APPLICANT: Green, Bruce A.  
APPLICANT: Brinton, Jr., Charles C.  
TITLE OF INVENTION: Sequence and Analysis of LKP P11n  
Patent No. 5834187  
Patent No. 5834187 5786143  
TITLE OF INVENTION: Structural Gene and the LKP P11 Operon of No. 5834187 5786  
TITLE OF INVENTION: Haemophilus Influenzae  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: Massachusetts  
COUNTRY: US  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/473,750  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/277,321  
FILING DATE: 19-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Carroll, Alice O.  
REGISTRATION NUMBER: 33,542  
REFERENCE/DOCKET NUMBER: ACC94-02B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-861-6240  
TELEFAX: 617-861-9540  
INFORMATION FOR SEQ. ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 741 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-473-750-7

Query Match 20.0%; Score 6; DB 2; Length 741;  
Best Local Similarity 100.0%; Pred. No. 79;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TARIGE 10  
| | | | |  
Db 157 TARIGE 162

Search completed: July 31, 2002, 15:04:07  
Job time: 22 sec

**This Page Blank (uspto)**



L7 ANSWER 26 OF 36 MEDLINE  
 AN 1999182371 MEDLINE  
 DN 99182371 PubMed ID: 10082470  
 TI Activation of receptor for advanced glycation end products: a mechanism for chronic vascular dysfunction in diabetic vasculopathy and atherosclerosis.  
 AU Schmidt A M; Yan S D; Wautier J L; Stern D  
 CS Division of Surgical Science, Department of Surgery, College of Physicians & Surgeons of Columbia University, New York, NY 10032, USA.  
 SO CIRCULATION RESEARCH, (1999 Mar 19) 84 (5) 489-97. Ref: 89  
 Journal code: 0047103. ISSN: 0009-7330.  
 CY United States  
 DT Journal; Article; (JOURNAL ARTICLE)  
 General Review; (REVIEW)  
 (REVIEW, TUTORIAL)  
 LA English  
 FS Priority Journals  
 EM 199903  
 ED Entered STN: 19990402  
 Last Updated on STN: 19990402  
 Entered Medline: 19990324  
 AB Receptor for advanced glycation end products (**RAGE**) is a member of the immunoglobulin superfamily of cell surface molecules and engages diverse ligands relevant to distinct pathological processes. One class of **RAGE** ligands includes glycoxidation products, termed advanced glycation end products, which occur in diabetes, at sites of oxidant stress in tissues, and in renal failure and **amyloidoses**. **RAGE** also functions as a signal transduction receptor for **amyloid** beta peptide, known to accumulate in Alzheimer disease in both affected brain parenchyma and cerebral vasculature. Interaction of **RAGE** with these ligands enhances receptor expression and initiates a positive feedback loop whereby receptor occupancy triggers increased **RAGE** expression, thereby perpetuating another wave of cellular activation. Sustained expression of **RAGE** by critical target cells, including endothelium, smooth muscle cells, mononuclear phagocytes, and neurons, in proximity to these ligands, sets the stage for chronic cellular activation and tissue damage. In a model of accelerated atherosclerosis associated with diabetes in genetically manipulated mice, blockade of cell surface **RAGE** by infusion of a soluble, truncated form of the receptor completely suppressed enhanced formation of vascular lesions. Amelioration of atherosclerosis in these diabetic/atherosclerotic animals by soluble **RAGE** occurred in the absence of changes in plasma lipids or glycemia, emphasizing the contribution of a lipid- and glycemia-independent mechanism(s) to atherogenesis, which we postulate to be interaction of **RAGE** with its ligands. Future studies using mice in which **RAGE** expression has been genetically manipulated and with selective low molecular weight **RAGE** inhibitors will be required to definitively assign a critical role for **RAGE** activation in diabetic vasculopathy. However, sustained receptor expression in a microenvironment with a plethora of ligand makes possible prolonged receptor stimulation, suggesting that interaction of cellular **RAGE** with its ligands could be a factor contributing to a range of important chronic disorders.

**This Page Blank (uspto)**